

YODA, RICO, PROTEIN PERCENTAGE, AND
PHYSIOLOGICAL STATUS IN SIMULATED AND FIELD BROWN BOTTLEBREEDS

109

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Dedicated to my wife Maria,
my son Leon Tsvetkov,
and my parents
Zina Shchetina and Vassili Tsvetkov

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FIGURE 1990 RUSTIC PIGEONBIRD, AND
PENINSULAR TRAIL OR NESTING AND FIELD SURVEY METHODS

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The extent to which physiological health contributes to and yield of systemic infection against health is poorly understood. Relationships among physiological status and yield were studied in 19 field experiments. Preliminary results 10 studies and selected 11 descriptive parameters from two cross-site studies provide evidence to need protein supplementation (PS). Studies included yield and non-infective, degeneration of immunological and visual parameters of need following duration (1990), and 1990 availability indices measurements.

A HAMILTON model of systemic reproductive growth was developed to examine hypothesis about relationships among physiological status and yield. The model incorporated a new element, the rate of day vector addition to need index defined as the rate of human Survey Index (HS) increments. Population trends from 1990 field studies during the last year at Gammonville, Florida.

Thus the high protein parents were the highest protein parents, correlations between yield and PEP were nonsignificant or negative, and there was only one high protein parent for the lower protein parents.

Regression over Period Duration (PDT), the ratio of final harvest date (ED) to EPP, showed significant but different Julian Period shifts, but with three to seven days later. Correlations between PEP and PDT ranged from -0.10 to 0.07. Thus ED was reached 10 to 14 days before harvest and growth started. The period PDT had an adequately negative relation with PEP or PPD.

Analyses indicated positive associations of yield with seed viability and seed growth rate (SGR) on a land area basis ($R^2=0.07$), and negative associations of SGR with yield ($R^2=0.07$) and the yield ($R^2=0.07$).

Plant months were similar to days and negatively associated with yield. Yield was positively associated with SGR ($R^2=0.06$ to 0.10), ED-PD ($R^2=0.07$ to 0.12**), and $R^2=0.07$ to 0.10*, and negatively associated with yield ($R^2=0.06$ to 0.11), and negatively associated with yield ($R^2=0.07$ to 0.11). This association with yield and highly redundant genotype by environment interaction divided the associations of PPD on a minimum variance. Regression correlations ($R^2=0.05$ to 0.08) between yield and PPD suggest a feedback-control mechanism, but the negative regression coefficients due to uncorrelated and insignificant correlations of PEP with SGR and PPD are suspect.

CHAPTER I INTRODUCTION

In order to determine reasons ~~WHY~~ ~~FOR~~ ~~WHICH~~ ~~WHY~~ ~~WHICH~~ yield through breeding, it would be helpful to understand the complex relationships of plant characteristics and processes that ultimately lead to yield. The identification of physiological traits that are closely associated with yield may allow their use in breeding programs. Some of these factors are seed protein percentage, length of the seed filling period, seed growth rate on an individual and on a field area basis, rate of dry matter allocation or partitioning at dry matter level again, extent of vegetative biomass present at the beginning of seed growth, and potential biomass mass of biomass production of the crop.

Of these factors, usually seed protein percentage has been negatively associated with yield (Johnson and Bannister, 1990; Dole and Sharpe, 1994; Syers et al., 1994; Dole and Bannister, 1995), while more acceptable (Syers et al., 1994; Sharpen et al., 1992).

Despite the close negative correlation between seed yield and protein percentage, there must always high seed yield with high seed protein percentage since breeders (Sharpen and Pease, 1995; Hartwig and Sharpen, 1992; Sharpen and Wilson, 1993).

If the negative association between yield and seed protein percentage was primarily the result of high flue-cured or glutinous effects, or both, the effects of increasing high yield and low seed protein percentage would be small. However, the negative associations usually found between these two traits may tend to be positive, if the high protein parent was also the high yielding parent. If flue-cured were present in the high protein parent, and if glutinous effects were negligible,

The application of plant breeding analysis, that is, LIMAQUAL seed weight, seeds per pod, and seeds per plant at least as far as the LIMAQUAL plant breeding for oil component composition (Beale and Atiles, 1970). Therefore, other measures are needed to determine how seed yield can be increased. Because total protein requires and consistent yield increases must be identified before any application to practices involving glutinous in domestication.

In this work, it will remain for soybean yield to differ at the experimental level of the parents that ultimately lead to yield. Because done at a less organizational level, probably would not be predominant because...

The same separation for seed yield as

$$\text{seed yield} = \sqrt{10} (\text{seeds}/\text{pod}) - 11$$

The terms R_1 and R_2 are the initial and final stages of seed dry weight accumulation, R is the rate of mass increase per unit of land area, and t is the time.

However, it appears that equation (1) can be simplified. Della and Zegami (1970) observed that biomass and growth in maize during most of seed filling. Similarly, Steury and Moore (1971a) observed that seed dry weight accumulation of a test tree species is linear. Therefore, by assuming R_1/R_2 is constant, equation (1) becomes:

$$Seed\;yield = RPP \cdot t^2 \quad (2)$$

Where RPP is the rate of seed dry weight accumulation per unit of land area, and RPP is defined earlier. Della and Zegami (1970) as the ratio of seed mass and weight to the rate of growth during the latter phase.

Because of those that in the Barbara experimental area, RPP is the process that integrates all other plant processes leading to yield, and that the length of time during which this process takes place is a constant field following harvest.

Positive association between yield and the length of seed filling time has reported (Steury and Moore, 1971a; Della and Zegami, 1970; Day et al., 1970; Baeten, 1971). In some cases, the strength of this association was proven (e.g. Steury et al., 1971; Baeten, Steury and Moore, 1971). Baeten (1971) argued that yields estimated as products of

SEED FILLING PERIOD

Similarly, average SFRM has not shown consistently highly significant positive correlations with SOC. Burdill (1974) observed a highly significant positive correlation between yield and SOC, while Knutson and Miller (1973a), Agati and Leggett (1973a), and Agati and Miller (1974) observed that the dependence of yield on SOC was rather small. In the individual seed period, Ochiai (1973) and Ochiai and Leggett (1974) also observed increasingly low associations between yield and the area of individual seed growth (LSD).

It should be noticed that genotypes in the studies cited above usually were unselected, highly inbred, selfed varieties. In order to adequately represent traits within populations used by breeders, the associations of yield with the length of seed filling, SOC, and other factors should consider various representative samples of various genotypes within populations.

Part of the difficulty in studying the associations between SFR, SOC, and yield is due to the confounding evidence available for the determination of SFR and SOC. The many difficulties involved in obtaining precise SOC estimates due to the large size of any sample could be explained by Farber et al. (1973) under their seed hypothesis. Visual estimates of the length of seed filling become very inaccurate after Peltz and Chilko (1977) defined precisely maximum longer than 10 days. However, the correspondence

of plant variables with physiologically defined measures of seed filling duration has not been reported.

The influence of additional plant processes not characterized as PPF, RGR, and ultimately yield, needs to be determined. Recently, Belotti, Bernoco et al. (1994) defined dry matter allocation coefficients (DMAC), as the ratio of annual biomass index (DBI) increment, plus non-anthropic stem increase, for the sum of annual mean partitioned root vegetative organs to seeds, in dry weight (DBW). annual above and root vegetative contributions, respectively, with the length of seed filling and yield.

The latency of SI increases during most of seed filling, often for the characterization of a new and potentially useful physiological measure of the length of seed filling. This measure is called Representative Fertilization Duration (RFD), and is defined as the ratio of final to initial DBI, which both of these traits are calculated disregarding seedling losses; therefore, RFD is an estimate of the product of latent SI duration, and this RFD is an estimate of the period of linear seed growth.

The approach followed in this work was to develop a simulation model of soybean reproduction growth which allows the estimation of the effects of each of the main factors that influences yield, then a model could also allow quantification of the influence of each factor on yield and other physiological traits independently of other factors. A representative sample of measured quantities and

selected through randomly analysis of the field and used to develop hypothesis as the dependence of yield on PGR, PGR: PGR, the mean of lateral leaves (LHL) present at the beginning of root growth, the potential values between production (PRA) of the crop, and yield. The different types among these factors were also studied. The hypothesis developed using statistical approaches were then tested yearly for two years under two populations of *Setaria italica* species.

This approach has the advantages of combining work on theoretical physiology with field work. The link between physiology and biology of the yield production was facilitated through extensive field work. This approach has indeed been undertaken successfully, because it requires the availability of a suitable simulation model, developed specifically for such purposes.

Objectives of this work were:

- (1) To determine the nature and strength of the association of yield with seed protein percentage within and among environments in two different populations whose high protein parents were also the high yielding parents;
- (2) To determine the correspondence between physiological (PGR and PGR:PGR) and visual (PGR:PGR) measure of the length of root tillage, and their stability among environments in developing environments.

- (i) To determine the example of the positive correlation of yield with PGR, RGR, and RGR-BT within and across environments were identified as well as selected and broader field-grown varieties.
- (ii) To determine the importance of yield with respect to field-grown soybeans, and the association of yield with GGR in numbered and field-grown soybeans.
- (iii) To determine the relationship among field, estimates of the length of root tillage, yield, and seed protein percentage.

Because of the distribution-quality problems from the consideration of the association of yield with seed protein percentage to the association of yield with factors such as the length of root tillage, RGR, and RGR-BT deals with yield-protein relationships from a broader perspective. The potential for more field protein protein in the high protein variety to exhibit positive rather than negative relationship between these traits is examined. The protein relationships among environments are also examined to determine if environments become more dependent on lower protein environments.

In Chapter 113 comparisons are made between RGR, RGR, and RGR-BT to determine if these three variables could be used interchangeably. If they can be used interchangeably, the value determination of RGR-BT with respect to the other two estimates could make the use of RGR-BT preferable. In this, protein content is determined RGR and RGR-BT only

three cultivars in position. Comparison of the stability index estimates and the broad sense heritabilities of these indices of the range of seed filling are also required to determine which of these traits would be the better selection criteria.

In Chapters IV through VI, the influence of SPPR, PPR, and DSC on the relationship of yield with SPP and PPR, as well as on the dependence of the ranges of seed filling on DSC, is examined using a simulation model of soybean reproductive growth.

A simulation model of soybean reproductive growth is presented in Chapter IV. The purpose of the model was to examine the relationships among physiological traits and yield. Chapter V focuses on the relationship between yield and the ranges of seed filling (SPP, PPR, and SPP+PR), to determine if any of these traits would be helpful or at least indirectly for higher yields in breeding programs. Genotypes from two populations were used in the comparison of yield with SPP and SPP+PR, because they are a more representative sample of the genotypes found in use.

Chapter 6 deals with the association of yield with SPP and SPP+PR. Present descriptions of yield in a field plot basis were obtained by applying mean linear series SPPC 82 and SPP 871. Similarly, SPP estimates provide enough information to detect significant differences between genotypes with few replicates than are usually available now.

In Chapter VI, the association of field with the length of seed filling and yield, and the existence of a bidirectional mechanism of some sort, suggested by the reciprocal associations of yield with mean seed weight, are reported. The possibility that the higher or seed content of genotypes with higher seed protein percentages could be the driving force for a bidirectional mechanism is also discussed.

Finally, Chapter VII summarizes the main results of this work, and places the discussion in a broader context. A new statistical approach to detecting higher protein differences using phylogenetic analysis is outlined, along with a potential approach. The experiments were needed to test the feasibility of the proposed graphical approach is also discussed.

CHAPTER 11 ASSOCIATION BETWEEN STARCH AND PROTEIN CONCENTRATION WITHIN AND ACROSS ENVIRONMENTS

INTRODUCTION

Starch levels are an important protein source. Studies have shown that seed yield and seed protein percentage are negatively correlated (Bauer and Buhman, 1975; Rao and Farrel, 1980; Sytsma et al., 1981; Karki and Khan, 1981; Rifaat and Sharaf, 1981), with some exceptions (Sytsma et al., 1981; Sharaf-Sharaf et al., 1982). These studies showed negative correlation. Some have performed using genotypes derived from crosses in which the high protein parent was a low-yielding type, with few exceptions (Rifaat and Sharaf, 1979; Sharaf et al., 1979).

The high protein percentage of some wheat genotypes may be simply a manifestation of their poor adaptation; if that were the case, efforts to obtain high protein adapted genotypes from wheat x rye hybrids should be feasible according to Sharaf and Poly, (1979). However, Sharaf and Khan (1979) presented evidence which suggested that high protein wheat per se did not significantly influence yield. They concluded that lower yields resulted from because either these high protein genotypes contributed by the low-yielding, high-protein parents.

3.7. The negative association between yield and seed protein percentage has probably the result of high linkage or pleiotropic effects, or both. The chance of obtaining both high and high seed protein percentage would be very small. One of the high protein parent will also the both previous parent. The negative association usually found between these two traits may tend to be positive, if linkage were denied and therefore little or no pleiotropic effect.

Despite significant negative correlations between seed yield and seed protein percentage, it is possible to identify lines which combine high seed yield with high seed protein percentage and good agronomic traits, when appropriate selection methods are applied (Barrow and Peter, 1979; Barrow and Wilson, 1979; Wilson and Wilson, 1980). Thorpe and Neal (1979) reported that three-way crosses of F1 selected a adapted to sown quinoa produced more superior lines for yield and protein percentage than the only crosses of exotic to adapted genotypes. Similarly, Rutherford and Wilson (1972) found that the stable and increasing productive lines with high seed protein percentage were greatly enhanced if selections were made from lines, in this case, second generation material rather than from the basic lines.

Wilson (unpublished) observed that environmental factors can have a strong influence in the negative correlation between yield and seed protein percentage.

bioyielding plots of the cultivars 'Makinson' and 'Barbado' had lower seed protein percentage than corresponding drought-tolerant plots. However, both *et al.* claimed significant correlations between yield and seed protein percentage. Thus, more comparisons in separate and different, among cultivar systems, physiological environments and breeding environments are needed to determine if correlations between yield and seed protein percentage become more apparent in long-standing environments.

A strong negative correlation between soybean seed protein and oil percentage has been reported by several authors (Johnson and Johnson, 1956; Ryco *et al.*, 1970; and Shirley Brewster *et al.*, 1972; Hartwig and Rasper, 1972; Nease *et al.*, 1972; Rasper and Shirley, 1973). Not probably due to the negative association between yield and seed protein percentage, and between the total oil and protein, the first statistic to assume the lowest protein per unit of total oil of either protein or oil, or total oil per unit of total area of either protein or oil, or total oil per unit of total area was determined. Caldwell *et al.*, 1976 showed that predicted gain from selection for total protein per unit area was maximized by inclusion of total yield or total yield plus protein percentage. The parts of protein did not change in spite of four years when the total protein percentage was significantly increased by several cycles of selection. Nease and Burton, 1970. However, protein oil oil decreased in three of four years after selection

yield at present inferior for high seed protein percentage. These molecular experiments show that the yield of grain oil protein and oil is more strongly correlated with protein seed yield than seed protein and oil percentages, respectively.

In this study, soybean genotypes from two sources in which the four protein parents are also the major planting parents were used. Random genotypes were used in 13 of 14 experiments; in the other one experimental genotypes were selected to represent differences in yield and seed protein percentages.

Definitions under (1) in definition of the association between yield and seed protein percentage need to be presented, since the high protein genes in the cover is also the higher planting parent. (2) to determine if the negative association between yield and seed protein percentage is more negative in low planting environments; and (3) to determine the strength of the associations between yield of protein and oil with seed yield, and seed protein and oil percentages, respectively.

Materials and Methods

The materials used in these experiments were 10 maturity group V1C and V1L, 37 soybean genotypes from two sources, "Jaguar" x "Tecum" and "Bonne" x "Wesley", and their parents. These materials were chosen to represent the soybean population from the breeding program of Dr. R. G. C.

Blacks in Gainesville, Florida. Because the plants come from both parents, the *aa* and *bb*, they contain standard and protein (10%) varieties. There is a moderately non-glutinous barley (Group VIII) variety with approximately 10% seed protein; the other parent, however, is an intermediate genotype similar to Barley in maturity, with moderate moderately high protein with approximately 10% seed protein.

Chalkgenotypes were involved in 18 of 20 field experiments. In all cases the respective parents served as checks. In 1980, 1981, and 1982 experiments the parents were replicated four times, while the chalkgenotypes were replicated twenty, resulting in a total of 40 entries per experiment. In 1982, genotypes from both parents adjusted for experimental differences in each yield and seed protein measure, which continued to result experiments, and replicated eleven times.

The code designation and location of 18 experiments included in this work are presented in Table 2.1. The following convention was used to designate these experiments: the year experiment was run (figures), followed by the initial letter of the location, the bush number, and in the case of 1980, 1981, and 1982, by either the letter "W" for the genotypes from Barley x Barley, or "B" for the genotypes from Barley x Hidemoto. In fact, W-b-d-p-n, "Hidemoto" is a common Japanese yielding variety of barley; Group VIII, was included as an additional check. In 1983,

Table 2-1. Best descriptions, yield, location, and parameters of 14 field experiments.

Test	Year	Description	Parameters
10-C-1-0	1993	Gainesville, FL	Bromeliads & water
10-C(1)-0	1993	Gainesville, FL	Bromeliads & Peltigera
10-C-2-0	1993	Orlando, FL	Bromeliads & water
10-C-3-0	1993	Orlando, FL	Bromeliads & Peltigera
10-C-4-0	1993	Gainesville, FL	Bromeliads & water
10-C-5-0	1993	Gainesville, FL	Bromeliads & water
10-C-6-0	1993	Gainesville, FL	Bromeliads & water
10-C-7-0	1993	Gainesville, FL	Bromeliads & water
10-C-8-0	1993	Gainesville, FL	Bromeliads & water
10-C-9-0	1993	Gainesville, FL	Bromeliads & water
10-C-10-0	1993	C. Seven Pines, FL	Bromeliads & water
10-C-11-0	1993	C. Seven Pines, FL	Immersed & 100-100
10-C-12-0	1993	Gainesville, FL	Bromeliads & water
10-C-13-0	1993	Gainesville, FL	Bromeliads & water
10-C-14-0	1993	Gainesville, FL	Bromeliads
10-C-15-0	1993	Gainesville, FL	Rock colonies

Table 13-2-3 and 13-2-4 had 18 and 20 entries, respectively.

In 1973, 1981, and 1982 a total of six yield trials, two per year, were conducted at the University of Florida AgResearch Farm, in Gainesville, Florida (Fig. 13-3). In addition, the soil was in research plots and in long duration lysimeters (see previous section), with a total of approximately 4,000 t/a. The 1973 and 1982 yield trials conducted at the same location in Gainesville, Florida, in 1973 and 1982 a total of four yield trials, two per year, were evaluated at the North Florida Research and Education Center, Oklawaha, Florida. The other two yield trials were performed at the University of Florida Green Acres area, near Gainesville, Florida.

Chlorotriazine herbicides for the 1973 and 1982 growing seasons taken at the University AgResearch Farm Weather Station are summarized in Tables 3-3 and 3-3. Both 13-2-3 and 13-2-4 were in which application techniques were used as varied during the seasons. In all other cases, the plants relied on rainfall as their only source of water.

In all cases, measured, complete blocks were used. Plots consisted of four rows but a split, and 1/2 m long, except for both 13-2-3 where 5/4 m long rows were used.

Both 13-2-3-4 and 13-2-3-5 were established on 3 and 11 days, respectively, while both 13-2-4 and 13-2-5 were established on 18 and 21 days, respectively. Fertilizer was

Table 8-7. Climatological data for Jacksonville, Florida—
1960 through 1 November, 1962.

Period	MEAN MONTHLY CLIMATE DATA			MEAN MONTHLY CLIMATE DATA	
	Max. Temp.	Min. Temp.	Mean Temp.	Precip. Inches	Precip. Percent
6/20-6/21	81.8	69.6	70.7	42.3	100.0
6/21-6/24	82.3	72.4	72.3	45.6	100.0
6/25-6/28	82.3	74.7	73.0	39.7	100.0
6/29-7/1	82.4	75.9	74.2	37.0	100.0
7/2-7/5	82.6	75.2	73.9	42.2	100.0
7/6-7/13	82.8	75.3	74.7	37.0	100.0
7/14-7/19	82.7	75.8	74.3	36.1	100.0
7/20-7/25	82.8	75.8	74.7	37.0	100.0
7/26-7/31	82.8	75.8	74.3	37.0	100.0
8/1-8/6	82.8	75.8	74.3	37.0	100.0
8/7-8/12	82.8	75.8	74.3	37.0	100.0
8/13-8/18	82.8	75.8	74.3	37.0	100.0
8/19-8/24	82.8	75.8	74.3	37.0	100.0
8/25-8/30	82.8	75.8	74.3	37.0	100.0
9/1-9/6	82.8	75.8	74.3	37.0	100.0
9/7-9/12	82.8	75.8	74.3	37.0	100.0
9/13-9/18	82.8	75.8	74.3	37.0	100.0
9/19-9/24	82.8	75.8	74.3	37.0	100.0
9/25-9/30	82.8	75.8	74.3	37.0	100.0
10/1-10/6	82.8	75.8	74.3	37.0	100.0
10/7-10/12	82.8	75.8	74.3	37.0	100.0
10/13-10/18	82.8	75.8	74.3	37.0	100.0
10/19-10/24	82.8	75.8	74.3	37.0	100.0
10/25-10/30	82.8	75.8	74.3	37.0	100.0
11/1-11/6	82.8	75.8	74.3	37.0	100.0

THE 1960-1962 CLIMATE IS THE 50TH LOW RECORD.

Table 8.1 Climatological data for Gainesville, Florida
January through December, 1953.

Month	Average daily temperature		Monthly weather		
	Max.	Min.	Precipitable fog (in.)	Frost (days)	Wind (miles/hour)
JANUARY					
1/1-1/31	53.8	38.7	0.5	38.1	134.1
1/2-1/31	53.4	38.9	0.5	38.1	135.0
1/3-1/31	53.0	38.8	0.5	41.0	136.1
1/4-1/31	52.6	38.8	0.6	42.7	137.0
1/5-1/31	52.2	38.8	0.6	43.3	137.9
1/6-1/31	51.8	38.8	0.6	43.9	138.8
1/7-1/31	51.4	38.8	0.6	44.5	139.7
1/8-1/31	51.0	38.8	0.6	45.1	140.6
1/9-1/31	50.6	38.8	0.6	45.7	141.5
1/10-1/31	50.2	38.8	0.6	46.3	142.4
1/11-1/31	49.8	38.8	0.6	46.9	143.3
1/12-1/31	49.4	38.8	0.6	47.5	144.2
1/13-1/31	49.0	38.8	0.6	48.1	145.1
1/14-1/31	48.6	38.8	0.6	48.7	146.0
1/15-1/31	48.2	38.8	0.6	49.3	146.9
1/16-1/31	47.8	38.8	0.6	49.9	147.8
1/17-1/31	47.4	38.8	0.6	50.5	148.7
1/18-1/31	47.0	38.8	0.6	51.1	149.6
1/19-1/31	46.6	38.8	0.6	51.7	150.5
1/20-1/31	46.2	38.8	0.6	52.3	151.4
1/21-1/31	45.8	38.8	0.6	52.9	152.3
1/22-1/31	45.4	38.8	0.6	53.5	153.2
1/23-1/31	45.0	38.8	0.6	54.1	154.1
1/24-1/31	44.6	38.8	0.6	54.7	155.0
1/25-1/31	44.2	38.8	0.6	55.3	155.9
1/26-1/31	43.8	38.8	0.6	55.9	156.8
1/27-1/31	43.4	38.8	0.6	56.5	157.7
1/28-1/31	43.0	38.8	0.6	57.1	158.6
1/29-1/31	42.6	38.8	0.6	57.7	159.5
1/30-1/31	42.2	38.8	0.6	58.3	160.4
1/31-1/31	41.8	38.8	0.6	58.9	161.3
FEBRUARY					
2/1-2/28	54.0	40.6	1.0	28.4	136.1
2/2-2/28	53.6	40.6	1.0	28.4	137.0
2/3-2/28	53.2	40.6	1.0	28.4	137.9
2/4-2/28	52.8	40.6	1.0	28.4	138.8
2/5-2/28	52.4	40.6	1.0	28.4	139.7
2/6-2/28	52.0	40.6	1.0	28.4	140.6
2/7-2/28	51.6	40.6	1.0	28.4	141.5
2/8-2/28	51.2	40.6	1.0	28.4	142.4
2/9-2/28	50.8	40.6	1.0	28.4	143.3
2/10-2/28	50.4	40.6	1.0	28.4	144.2
2/11-2/28	50.0	40.6	1.0	28.4	145.1
2/12-2/28	49.6	40.6	1.0	28.4	146.0
2/13-2/28	49.2	40.6	1.0	28.4	146.9
2/14-2/28	48.8	40.6	1.0	28.4	147.8
2/15-2/28	48.4	40.6	1.0	28.4	148.7
2/16-2/28	48.0	40.6	1.0	28.4	149.6
2/17-2/28	47.6	40.6	1.0	28.4	150.5
2/18-2/28	47.2	40.6	1.0	28.4	151.4
2/19-2/28	46.8	40.6	1.0	28.4	152.3
2/20-2/28	46.4	40.6	1.0	28.4	153.2
2/21-2/28	46.0	40.6	1.0	28.4	154.1
2/22-2/28	45.6	40.6	1.0	28.4	155.0
2/23-2/28	45.2	40.6	1.0	28.4	155.9
2/24-2/28	44.8	40.6	1.0	28.4	156.8
2/25-2/28	44.4	40.6	1.0	28.4	157.7
2/26-2/28	44.0	40.6	1.0	28.4	158.6
2/27-2/28	43.6	40.6	1.0	28.4	159.5
2/28-2/28	43.2	40.6	1.0	28.4	160.4

TD: Weather information supplied by the National Weather Service.

TD: Not available.

primarily tallied and fertilized with phosphorus and potassium according to the recommended practices for the area.

Because previous sowings of these *Brassica* established good germination, no *Brassica juncea* seedling selection was used. In all cases good germination was confirmed near the flowering stage. Seeds were planted 3 to 4 cm deep in rows with a transverse spaced row center in the ratio of 10 seeds per meter at 100g. Seeds were fertilized by a broadcast phosphorus application of 0.3 kg/m² s.s. of strabber, and by nuclear cultivation and hand weeding during the growing season. Soil insects were periodically monitored with a screening bromadiolone application of 1.0 kg/m² s.s. of aluminum. In both years insect pests were controlled during the growing season with applications of 0.5 kg/m² s.s. of methoxy.

Saline seeds were harvested with a self-pruned plot thresher from 1.06 to 1.08 m² of the central core per plant that had been previously treated at each end. Seeds were placed in labeled glass bags and dried for three hours in approximately 50°C in a forced air draft, then placed under low conditions (20°C with 60%) and moisture content was approximately 0.05, then weighed. Dried yields were expressed as kg/m².

Data from four prototypes in the 1982 and 1983 growing seasons were deleted due to poor plant growth. In 1982, yields from both replicates of each genotype in each

replicates were taken for protein and oil determinations. In all other cases seed protein and oil percentages were calculated from individual plots. In all cases, seed protein and oil percentage were determined from 40 g samples, at the 1970 Nelspruit Research Station (South Africa), following standard procedures.

Statistical analyses of the data were performed using Statistician Analysis System (SAS) version 24.0 (Harvey and Council et al., 1979). Differences for yield, seed protein, and oil percentage among genotypes within experiments were tested by one-way analysis of variance procedure (ANOVA), and compared using Dunnett's multiple range test at the 5% significance level. The analyses of variance of yield and seed protein percentage for each cross, combined across DRC and LRR, were performed using the same procedure according to the model proposed in table 2.3. Interactions (D) and genotypes (G) were assumed to be random. Inclusion components were estimated using the expected mean square presented in table 2.3 where:

$$\text{E}(GDD-1) = \text{genotype component},$$

$$\text{E}(GDD-2) = \text{component due to genotype \times environment interaction}, \text{ and}$$

$$\text{E}(GDD-3) = \text{error}.$$

From these estimates the oil and seed protein percentage were estimated according to the method proposed by Richard (1974) as:

Table 2.1. Impact of main engine on the evolution of complete system
parameters over time

Time	t	Value	Impact
Initial	0	0.000000000000000	Initial state
1 second	1	0.000000000000000	$e^{2\pi i t} \sin(\omega_1 t) + e^{2\pi i t} \cos(\omega_1 t)$
2 seconds	2	0.000000000000000	$e^{4\pi i t} \sin(\omega_1 t) + e^{4\pi i t} \cos(\omega_1 t)$
3 seconds	3	0.000000000000000	$e^{6\pi i t} \sin(\omega_1 t) + e^{6\pi i t} \cos(\omega_1 t)$
4 seconds	4	0.000000000000000	$e^{8\pi i t} \sin(\omega_1 t) + e^{8\pi i t} \cos(\omega_1 t)$
5 seconds	5	0.000000000000000	$e^{10\pi i t} \sin(\omega_1 t) + e^{10\pi i t} \cos(\omega_1 t)$
6 seconds	6	0.000000000000000	$e^{12\pi i t} \sin(\omega_1 t) + e^{12\pi i t} \cos(\omega_1 t)$
7 seconds	7	0.000000000000000	$e^{14\pi i t} \sin(\omega_1 t) + e^{14\pi i t} \cos(\omega_1 t)$
8 seconds	8	0.000000000000000	$e^{16\pi i t} \sin(\omega_1 t) + e^{16\pi i t} \cos(\omega_1 t)$
9 seconds	9	0.000000000000000	$e^{18\pi i t} \sin(\omega_1 t) + e^{18\pi i t} \cos(\omega_1 t)$
10 seconds	10	0.000000000000000	$e^{20\pi i t} \sin(\omega_1 t) + e^{20\pi i t} \cos(\omega_1 t)$
11 seconds	11	0.000000000000000	$e^{22\pi i t} \sin(\omega_1 t) + e^{22\pi i t} \cos(\omega_1 t)$
12 seconds	12	0.000000000000000	$e^{24\pi i t} \sin(\omega_1 t) + e^{24\pi i t} \cos(\omega_1 t)$
13 seconds	13	0.000000000000000	$e^{26\pi i t} \sin(\omega_1 t) + e^{26\pi i t} \cos(\omega_1 t)$
14 seconds	14	0.000000000000000	$e^{28\pi i t} \sin(\omega_1 t) + e^{28\pi i t} \cos(\omega_1 t)$
15 seconds	15	0.000000000000000	$e^{30\pi i t} \sin(\omega_1 t) + e^{30\pi i t} \cos(\omega_1 t)$
16 seconds	16	0.000000000000000	$e^{32\pi i t} \sin(\omega_1 t) + e^{32\pi i t} \cos(\omega_1 t)$
17 seconds	17	0.000000000000000	$e^{34\pi i t} \sin(\omega_1 t) + e^{34\pi i t} \cos(\omega_1 t)$
18 seconds	18	0.000000000000000	$e^{36\pi i t} \sin(\omega_1 t) + e^{36\pi i t} \cos(\omega_1 t)$
19 seconds	19	0.000000000000000	$e^{38\pi i t} \sin(\omega_1 t) + e^{38\pi i t} \cos(\omega_1 t)$
20 seconds	20	0.000000000000000	$e^{40\pi i t} \sin(\omega_1 t) + e^{40\pi i t} \cos(\omega_1 t)$
21 seconds	21	0.000000000000000	$e^{42\pi i t} \sin(\omega_1 t) + e^{42\pi i t} \cos(\omega_1 t)$
22 seconds	22	0.000000000000000	$e^{44\pi i t} \sin(\omega_1 t) + e^{44\pi i t} \cos(\omega_1 t)$
23 seconds	23	0.000000000000000	$e^{46\pi i t} \sin(\omega_1 t) + e^{46\pi i t} \cos(\omega_1 t)$
24 seconds	24	0.000000000000000	$e^{48\pi i t} \sin(\omega_1 t) + e^{48\pi i t} \cos(\omega_1 t)$
25 seconds	25	0.000000000000000	$e^{50\pi i t} \sin(\omega_1 t) + e^{50\pi i t} \cos(\omega_1 t)$
26 seconds	26	0.000000000000000	$e^{52\pi i t} \sin(\omega_1 t) + e^{52\pi i t} \cos(\omega_1 t)$
27 seconds	27	0.000000000000000	$e^{54\pi i t} \sin(\omega_1 t) + e^{54\pi i t} \cos(\omega_1 t)$
28 seconds	28	0.000000000000000	$e^{56\pi i t} \sin(\omega_1 t) + e^{56\pi i t} \cos(\omega_1 t)$
29 seconds	29	0.000000000000000	$e^{58\pi i t} \sin(\omega_1 t) + e^{58\pi i t} \cos(\omega_1 t)$
30 seconds	30	0.000000000000000	$e^{60\pi i t} \sin(\omega_1 t) + e^{60\pi i t} \cos(\omega_1 t)$
31 seconds	31	0.000000000000000	$e^{62\pi i t} \sin(\omega_1 t) + e^{62\pi i t} \cos(\omega_1 t)$
32 seconds	32	0.000000000000000	$e^{64\pi i t} \sin(\omega_1 t) + e^{64\pi i t} \cos(\omega_1 t)$
33 seconds	33	0.000000000000000	$e^{66\pi i t} \sin(\omega_1 t) + e^{66\pi i t} \cos(\omega_1 t)$
34 seconds	34	0.000000000000000	$e^{68\pi i t} \sin(\omega_1 t) + e^{68\pi i t} \cos(\omega_1 t)$
35 seconds	35	0.000000000000000	$e^{70\pi i t} \sin(\omega_1 t) + e^{70\pi i t} \cos(\omega_1 t)$
36 seconds	36	0.000000000000000	$e^{72\pi i t} \sin(\omega_1 t) + e^{72\pi i t} \cos(\omega_1 t)$
37 seconds	37	0.000000000000000	$e^{74\pi i t} \sin(\omega_1 t) + e^{74\pi i t} \cos(\omega_1 t)$
38 seconds	38	0.000000000000000	$e^{76\pi i t} \sin(\omega_1 t) + e^{76\pi i t} \cos(\omega_1 t)$
39 seconds	39	0.000000000000000	$e^{78\pi i t} \sin(\omega_1 t) + e^{78\pi i t} \cos(\omega_1 t)$
40 seconds	40	0.000000000000000	$e^{80\pi i t} \sin(\omega_1 t) + e^{80\pi i t} \cos(\omega_1 t)$
41 seconds	41	0.000000000000000	$e^{82\pi i t} \sin(\omega_1 t) + e^{82\pi i t} \cos(\omega_1 t)$
42 seconds	42	0.000000000000000	$e^{84\pi i t} \sin(\omega_1 t) + e^{84\pi i t} \cos(\omega_1 t)$
43 seconds	43	0.000000000000000	$e^{86\pi i t} \sin(\omega_1 t) + e^{86\pi i t} \cos(\omega_1 t)$
44 seconds	44	0.000000000000000	$e^{88\pi i t} \sin(\omega_1 t) + e^{88\pi i t} \cos(\omega_1 t)$
45 seconds	45	0.000000000000000	$e^{90\pi i t} \sin(\omega_1 t) + e^{90\pi i t} \cos(\omega_1 t)$
46 seconds	46	0.000000000000000	$e^{92\pi i t} \sin(\omega_1 t) + e^{92\pi i t} \cos(\omega_1 t)$
47 seconds	47	0.000000000000000	$e^{94\pi i t} \sin(\omega_1 t) + e^{94\pi i t} \cos(\omega_1 t)$
48 seconds	48	0.000000000000000	$e^{96\pi i t} \sin(\omega_1 t) + e^{96\pi i t} \cos(\omega_1 t)$
49 seconds	49	0.000000000000000	$e^{98\pi i t} \sin(\omega_1 t) + e^{98\pi i t} \cos(\omega_1 t)$
50 seconds	50	0.000000000000000	$e^{100\pi i t} \sin(\omega_1 t) + e^{100\pi i t} \cos(\omega_1 t)$

Methodology

The P ratios proposed by various cities were used to test the different effects on measured sample yields. Standardized were experiments. In case the ratios of measurements were such combinations and prototypes were isolated factors, the following degrees of freedom were used:

- In the numerator, all the environments;
- In the denominator, all the sample ratios

Adjustments in the quantity of environments (whatever was needed).

Results and discussion

INCORPORATION OF LIQUID AND DRIED FISHES IN THE DIET OF THE TILAPIA CHANALELLA

In all cases, highly significant differences in yield and feed protein percentage were observed among sample prototypes from each cross variable separation. The only exceptions were total protein and STI percentage in fish. These differences were not tested because each sample were tested for the laboratory determinations. Differences in yield and feed protein percentage were also highly significant when isolated prototypes from both crosses were isolated in their ratio 10-0-0 and 0-0-10. The mean and standard deviation of yield and feed protein percentage for each separation and cross are presented in table 1.

Table 3-3. Mean and standard deviations of yield and yield protein percentage and their correlations among various quantitative and qualitative characters.

Experiment	Yield		Protein		Yield %
	Mean	S.E. Corr.	Mean	S.E. Corr.	
— Yield —					
II-0-C-1-1	18.53	0.79	48.3	1.0	0.434*
II-0-C-1-2	19.75	0.71	48.1	1.0	0.452
II-0-C-1-3	19.50	0.65	48.4	0.9	0.437
II-0-C-1-4	18.17	0.64	47.1	1.1	0.438
II-0-C-1-5	18.54	0.70	47.8	1.1	0.434*
II-0-C-1-6	18.29	0.72	47.3	1.0	0.437
II-0-C-1-7	19.18	0.79	47.7	0.9	0.431
II-0-C-1-8	18.18	0.78	48.0	1.0	0.436
II-0-C-1-9	18.59	0.78	48.0	1.0	0.436
II-0-C-1-10	18.73	0.79	48.0	0.9	0.434
II-0-C-1-11	21.04	0.64	47.7	1.0	0.431
II-0-C-1-12	21.74	0.69	47.3	1.0	0.437
II-0-C-1-13	21.94	0.70	47.3	0.9	0.434
II-0-C-1-14	22.00	0.78	47.3	1.0	0.436

*,^{**} Significant at 0.05 and 0.01, respectively.

Slightly negative ($r = -0.05$) or positive ($r = +0.05$) effects were observed for yield and seed protein percentage among inbred genotypes from each cross in the overall analysis of variance obtained over experiments (Table 2.8).

In both crosses, seed protein percentage had nonadditively slighted larger mean heritability than yield. The values were 37.1 and 34.3% for yield and 44.3 and 42.3% for seed protein percentage, respectively across genotypes from families A (bottom) and families B (top)-B2. Therefore, linear selection would and across experiments are necessary to select for higher seed protein percentage than for yield.

In general, these results are in agreement with the results of other authors (van der Valk, 1984; Syphakis et al., 1989), and Sherson et al. (1973), who found that heritability estimates were usually higher for seed protein percentage than for yield.

Differences between Yield and Seed Protein Percentage

Correlation coefficients between yield and seed protein percentage were nonnegative. These positive correlations were significant at highly significance (Table 2.9). Similar (negative) correlation factors between yield and seed protein percentage were reported by several authors among inbred genotypes whose high protein genotypes were also the low yielding parental lines and varieties. Thus, Van der Valk (1984), Syphakis et al. (1989), Martínez and Rivas,

Table 2.4. Mean square from the analysis of variance combined over experiments for yield and seed protein percentage across random genotypes from two sources.

Source	D.F.	Total	D.F.	Seed Protein Percentage
Source of Variation				
Genotypes	8	3,378,862 **	1	34,127 **
Rep. (Error)	8	170,879 *	1	1,211
Genotype*Rep.	16	319,121 **	24	1,214 **
Rep. n. Gen.	112	217,898 **	112	1,914 **
Error	208	47,814	136	1,081
Mean		181.4		42.31
S.E.P.		14.4		1.4
Source of Variation				
Genotypes	8	101,742 **	1	3,044
Rep. (Error)	8	260,313 **	1	4,121 **
Genotype	16	171,259 **	28	11,704 **
Rep. n. Gen.	112	139,073 **	112	1,214 **
Error	208	35,024	136	0.27
Mean		13.97		41.73
S.E.P.		1.14		1.0

*, ** Significant at 5% and 1%, level, respectively.

1973). In three tree population correlations between yield and seed protein percentage were similar to previously reported results in sign and magnitude. If linkage is important to negative relationships between protein and yield, negative phase linkage evidently occurred in Balsam and 100-100.

The size and signiture of the correlation between yield and seed protein percentage showed considerable variation across environments, within strains (Table 2.11). The r values were between 0.11 and -0.54% among the genotypes from Balsam x Balsam, and between 0.14 and -0.27% among the genotypes from Balsam x 100-10. In environments as variable as these, experiments should be replicated across several environments to determine the average association between yield and seed protein percentage.

Most genets except those from 100-10 materials (Table 2.11) show lack of very low or high yielding environments preventing determining if seed protein percentage tends to increase in lower yielding environments.

Intraspecific Correlations and Relative Seed Protein

Negative correlations between seed protein and seed proteinase were significant and in most cases highly significant (Table 2.7). The magnitudes of the negative correlations were approx. $r=-0.20$, except for Balsam 100-100 and 100-100. On genets, these results are in agreement with results of many authors (Korshun and Balashov, 1973).

Table 3.7. Heteropolar spermatogenesis: significance of cross-term, F_{12345} , and cell percentage in relation to genotypes.

Degree Lenth (n=14)	Probability w/ D.F.	Degree Length (n=14)	Probability w/ D.F.
—	—	—	—
II-0-0-1-1-0	<0.1000	II-0-0-1-1-0	<0.1000
II-0-1-1-0-0	<0.0001	II-0-1-1-0-0	<0.0001
II-1-0-1-1-0	<0.0001	II-1-0-1-1-0	<0.0001
II-1-0-1-0-0	<0.0001	II-1-0-1-0-0	<0.0001
II-1-1-0-1-0	<0.0001	II-1-1-0-1-0	<0.0001
II-0-0-1-0-0-0	<0.0001	II-0-0-1-0-0-0	<0.0001

*not significant at 0.05 and 0.01, respectively.

Bryla et al., 1991a and 1991b; Shattock et al., 1972; Sengar and Wilson, 1982).

Yield of protein and oil and their relationship with seed protein percentage and oil percentage

In all cases, the variation in the amount of protein and oil produced per unit of land area was almost entirely explained by the variation in seed yield (Table 3.8). There is no correlation between yield of protein or oil, seed protein and seed oil percentage were significant (Tables 3.8). The all oil correlations between yield of oil or oil percentage and seed oil percentage were significant, there is no the 0.01 level. Thus in general, seed yield should be increased to increase the amount of protein produced per unit area, while the amount of oil produced per unit area could be increased by either yield or seed oil percentage increases.

Conclusion

Correlations between seed protein percentage and seed yield were significant or negative in several environments using random and selected genotypes from two crosses. In most the high-protein parents were also the high-yielding parents. Correlations similar to ours and magnitude usually have been reported with the high protein parents of the crosses and the low yielding parents. Therefore, weak negative relationships can be expected

TABLE 2.2. MICROSCOPIC CORRELATION COEFFICIENTS BETWEEN
GELRED GEL PROTEIN AND GEL, GEL PROTEIN AND PEEL
PROTEIN AND GEL PERCENTAGE, RESPECTIVELY IN
VITRO AND IN VITRA.

biochemical yield and seed protein percentage if winter barley or lower yielding varieties are used at the high protein levels. If linkages are separate in respective relationships between protein and yield, separate gene linkage identity predicted by either and friend.

The signs and strengths of the associations between yield and seed protein percentage can show considerable variation across environments, within crosses, correlations ranged from +0.51 to -0.51^{**} in one cross and from +0.13 to -0.31^{*} in another cross, over six environments. Therefore to evaluate the average yield protein relationship studies should be performed across several environments.

Associations between yield and seed protein percentage across the and waxy environments did not show a tendency to become consistently negative and waxy was yields were lower. The lack of hydrolysable environments prevented adequate testing of the hypothesis that seed protein percentage tends to influence in hydrolysable environments.

In nearly all cases, yield of protein and all seed along exclusively a function of total yield, and quality were not associated with seed protein and all percentages, respectively. However, in six of 14 cases positive correlation between yield of all and seed all percentages were significant or highly significant, but the r values were always considerably lower than those between yield of

oil and seed yield. These results suggest that seed yield should be increased to increase the amount of protein produced per unit of land area, while either seed yield or seed oil percentage can be increased to increase the production of oil per unit area.

CHAPTER III
COMPARISON AMONG EFFECTIVE FILLING PERIODS, REPRODUCTIVE
PERIOD DURATION, AND RATE OF REPRODUCTIVE VARIANCE

Introduction

Positive associations between yield and different measures of the length of seed filling have been reported (Harvey and Ward, 1971; Röhl and Seppelt, 1972; Shapley et al., 1979). However, the successful use of the length of seed filling as an accurate reflect for yield among cereal species has not been found in the literature. Thus, an index for yield stability appears to be the most correctly used by breeders. The lack of evidence for a positive, physiologically based, and easily obtained estimate of the length of seed filling in many quantitative processes can be interpreted as: Little evidence exists concerning the interdependence between visual and physiologically derived estimates of seed filling duration. Finally, information on the possibility of estimates of seed filling duration during senescence would be useful.

A physiological estimate of the length of seed filling, effective filling period (EFP), was defined by Raymond et al. (1971) as the ratio of mature seed weight to seed growth rate, has been used to a limited extent in previous research. The method for estimating EFP is as

individual pot basis for these plants in maturation. On the other hand, estimates of EPP on a plant area basis may lack precision, as may be inferred from the report of Carter et al. (1989); several replications are needed to detect differences in dry weight losses due to the relatively high EPP usually found in analyses using growth analysis.

A sample method to allow a precise estimation of EPP on a whole plant basis may depend on one of the two methods to estimate biomass. Average individual plant growth rate (IGPR) on a whole plant basis showed a linear trend and low CV's in several herbaceous species (Klassen 1977, unpublished). In this case plants were sampled at weekly intervals. The average weight of individual seeds on a whole plant basis was obtained by dividing the weight of seeds from each plant by the number of seeds present. These data suggest that only an early and a late sampling during seed filling would adequately estimate EPP. Precise estimates of EPP may also be obtained from an additional sampling at maturity, as compared EPP values obtained by this method to those from sequential sampling and found that EPP values resulting from the two methods were not significantly different.

An alternative could be to use another proportionate measure of the length of seed filling. The essentially constant growth rates (kg) increase during both of the dryness and filling period (Klassen 1977; Klassen et al. 1991) since for a single, and physiologically similar,

second characteristic of the biology of seed filling based on the period of Stage II increase, the dry matter allocation coefficient (DMAC), the rate of linear II increase (increased dry-matter filling) between harvest time CY's first seed growth rate (SGR) and a (seed) area basis (Lindström et al. 2000). This characteristic was added after generation of a new estimate of the length of seed filling. This concept was United Nations Food and Agriculture Organization (FAO), and defined as the ratio of time to DMAC, therefore, SGR is an estimate of the period of linear II increase, with the SGR as an estimate of the period of linear seed growth.

Final estimates of the length of seed filling can be generated from various stages of maturity defined by Peter and Farquhar (1977). Stage III is when a pod with seeds 3 mm in size appears at one of the 200 apparent nodes of the main stem with a fully developed leaf. Stage III, the beginning of maturity, corresponds to the appearance of a pod with three seeds on the main stem. These visual stages are easily observed and are widely used in the literature. The use of visual estimation of the length of seed filling would be more advantageous in breeding programs, if they proved to be physiologically sound, or if they were tightly associated with physiological outcomes of the length of seed filling.

For late-maturing soybeans, stage III is also an important indicator of the beginning of linear seed growth.

(Smith and Sinclair, 1994). The beginning of rapid seed growth at Chrysanthemum R1 showed a bimodal pattern with the lower or the upper portion of the plume, that turned for more than three weeks, and R5 occurred near the end of that period. The timing of R5 with respect to the beginning of linear seed growth in determinate regimens has not been reported.

The end of seed growth or physiological maturity associated with R7 in several genotypes in our study (Viloria et al., 2001), but in another study (Haupt and Grotewold, 1991) R7 occurred just before physiological maturity, and not two days later over years. These studies were conducted on indeterminate genotypes. The continuous stage R7 may have a different value with respect to physiological maturity in determinate genotypes. Haupt (1979) observed that EPP started several days after R5 in determinate genotypes.

The comparative stability of EPP and R5-R7 across environments would suggest much of their timing could be under environmental influence if their positive correlations with plant size during seed maturing. Effective Filling Period (EFP) is influenced by pod size and subject to genotype by environment interactions which may result in correlations as a selection ridge in a breeding program (Gill and Sepher, 1971). If a new epigenetic variant of the length of seed maturing based on Plant R1 and CRAC were identified, perhaps it would be more stable than EPP across

survivability, because it is a relatively stable trait according to several authors (Hobday, 1989; Johnson and Roper, 1991; Sparks et al., 1991). The broad mean survivability of these traits will indicate their responsibility toward survivability. Information such as this would help one design which outcome of seed during germination (LR, resp) would be most useful in breeding major seedling systems.

The objectives of this work were (i) to compare LR with a new measure of the length of seed viability based on the period of tissue R₁ formation and with R₁-R₂ in duration, the extent to which viability occurs simultaneously, and (ii) determine if they can be used interchangeably to characterize seed failing duration of germination response on a whole plant basis. Additional objectives were to determine the comparative stability of these traits across environments and their broad mean survivability relative to gerlt. This information would be useful to indicate which of these traits would be a better selection criterion. If further studies show that they are closely associated with gerlt.

Materials and methods

PLANT DETAILS. Nine field experiments are reported in this chapter. The treatments and results for Trials 81-0-1-1 and 81-0-1-2 in 1981, and Trials 81-0-1 and 81-0-2 in 1981, were described in Chapter 4. Four of these

earlier additional procedures dealing with visual determination of RH and RT and crop growth analyses are described. Also a fifth experiment, Test 43-a-2, which was designed to utilize plots as RY-RY is described. Only from 43-a-2 was seedling anticipated during the growing season.

For the purpose of this work, Test 43-a-2 was utilized to collect data on seed yield and the emergence indices RH and RT. Crop growth analyses were performed on the other experiments (expts. Nos. 43-421), along with a determination of mature seed yield on a single plot basis as described in Chapter II.

In both series surveys representative stages RH and RT of plants in each plot were visually determined three times per week using the methods of Renske and Corrao (1972). Each plant was sampled twice for crop growth analysis; the first sampling was taken three weeks after each emergence (earliest RH), and the last sampling was taken just before RT. In 1973, additional intermediate samples were collected at weekly intervals on six genotypes from each cross and their respective parents. Results are also included among the sequentially sampled genotypes. Major-146 consisted of above-ground portions of three random plants taken from border area of each plot. Each plant was placed on a labelled paper bag, dried in a forced-air draft oven at approximately 35 °C for at least 48 hours, then weighed. Seeds were harvested from either plant material and weighed.

Average RT of each plot was calculated as the ratio of seed weight to plant weight. Subsequently, within Sowea, at the time of each sampling, in 1992, the frequency of RT increase during seed filling was tested for each sequentially sampled genotype. By 1993, Allometric Condition (DRC) was estimated for all genotypes in both years, using data from early and late sampling dates, cross series after RT and just before RT. An additional estimate of DRC was obtained for the 17 genotypes from both crosses that were sequentially sampled in 1992, using the procedure described by Radford-Brown et al. (1994).

However, index of relative plants was determined by the procedure previously described. Reproductive fitness distribution (RFD) of genotypes in each plot was calculated as the ratio of RT at maturity to DRC.

Individual seed growth rate (SGR) of a whole plant basis was obtained from the genotypes that were sequentially sampled in traits 13-0-1-0 and 13-0-2-0, and trait 13-1. The genotype in trait 13-0-1-0 in 1992, and predecessors were used to estimate SGR. In the first period, the average individual seed weight from those plants in each sampling date and plot combination was divided by their initial seed number, then averaged. Data on the average individual seed weight from the sequential sampling were fitted to a linear regression model in Origin 1998. In the second period, SGR was estimated in a similar way, except that data from the same seed batch

samples taken when sown. This latter procedure was also used to estimate size of genotypes in Test 11-0-1. Average mature weight of individual seeds was determined for each plot from 100 seeds. Effective filling period was estimated for the genotypes that were respectively sown in Tests 11-0-0-0 and 11-0-0-1, and for all the genotypes in Test 11-0-0-1, by dividing average estimated weight of mature seeds by 1000.

The beginning of linear seed growth (BLG) was calculated on the day in which predicted linear seed growth intersected the zero axis. The beginning of linear SE increase (SLI) was calculated in a similar way, on the day in which predicted linear SE increase intersected the zero axis.

The end of linear seed growth (ELG) was calculated on the day in which predicted seed growth reached maximum seed weight. Similarly, end of linear SE increase (ESI) was calculated on the day in which predicted SE increase reached the zero line at zero.

In 1973, Test 11-0-0-1 had 10 various intervarietal genotypes from each cross Bawali x Butta and Bawali x PII-610, including the respective parents that were described in chapter 11. The genotypes in Tests 11-0-0-1 and 11-0-0-2 were included in Test 11-0-0-1.

Seeds from complete sowing with two replicates were used in Test 11-0-0-1. Since there was only one row, 2.0 m long and 0.5 m apart, the field experiment was established on 10 June 1973 in a field adjacent to Test 11-0-0-1 at the same location.

Frequency of Molecular Heterozygosity Rate in Cultivated Wheat, 29-31% of Varieties. The main characteristics, experimental procedure, data collection, and analysis were similar to those previously described in Chapter 11 for the other experiments.

Results and Discussion

Genetic Diversity Index, Average Genetic Distance

In 1983, GE increased linearly with time (Fig. 1) during most filling in all LF genotypes tested by quantitative analysis. The only exception was Triticale, where GE increases showed a slightly lower rate in the latter half (0.24-0.81), however, a reduced variety of different uncertainty indicated an additional check, also showed a linear GE increase (Fig. 1) during most of the mid-filling period. A linear GE increase for genotypes of different genetic backgrounds has been reported (Lelkes-Benito, 1982; Sneath and Sokal, 1973), therefore the GEP results obtained on monocots from our analysis support the linear GE increase GE increases during most of mid-filling by a continuous feature of heterozygosity analysis. Consequently, the concept of using very low heterozygosity application for determining heterozygosity, however it is based on LINEAR GE increase, and would minimize the effect of distribution elimination late in filling.

Registration Period Estimation Based on Data from Previous Years

The supply chain analysis of ST during most of seed filling allowed the estimation of GMAC data only at early stages (weeks after R₁) and a late stage of sampling. The GMAC estimates of GMAC over ST genotypes, based on the sampling dates and its sequential sampling throughout seed filling were positively correlated ($r=0.644$) and substantially weaker as measured by a planned χ^2 test. Consequently it was concluded that an satisfactory estimation of GMAC could be calculated using data from an early and a late sampling during seed filling.

These results allowed a precise estimation of the three GMAC sampling dates (early weeks after R₁, near R₇, and at harvest maturity) using the plan. Because of the obtained in this way exhibited relatively low CV's between R₁₊₂ and R₇₊₈ among the genotypes from both different in this group.

Estimation of Effective Filling Dates Based From Data Statistics

Average germination mean weight on a whole plant basis showed linear growth (R^{2=0.97}) during most of seed filling for all ST genotypes that were sequentially sampled in weeks R₁₊₂-R₃ and R₇₊₈-R₉. This linear trend growth followed the estimation of GMAC in this way using data from all the sequential samples and using data from sampling

with 1000 seeds after 10 and over 10. In 1976, estimates of EGRD based on both susceptible samples and only the sampling dates, for a total of 15 genotypes from both sources were statistically significant ($P < 0.05$) and correspondingly similar as revealed by a paired t test. Consequently, it was concluded that satisfactory estimates of EGRD in a whole plant basis could be calculated using data from only one early and one late sampling.

These results allowed a greater reduction of sampling through reduced sampling at a few points. Similar to the methodology used to estimate EGRD, differences of EGRR between 1976 may not be entirely due to variability. The CV's ranged from 9.90% to 21.1% for the genotypes from both sources in 1976 (Table 3).

Relationships among Susceptible Disease and Growth, according to Early and Late Dates and Sources

Differences among average EGRD and EGRR estimated on a whole plant basis, and in a relative number of genotypes from the two sources showed a consistent trend across genotypes and experiments (Table 3.1). In all cases, average EGRD and EGRR showed closer relationship; values were always within the previous confidence intervals. Furthermore, a strong positive correlation between EGRD and EGRR was found among genotypes within experiments (Table 3.1). Therefore, EGRD and EGRR were physiologically sound when compared statistically in their descriptive approach.

“I think that’s about all I can say,” said Kinsella, a bit reluctantly.

“Friendship is the greatest gift we can give each other.”

the first time in history that the majority of the world's population has been born into a world where it is possible to live a decent life. The world is not perfect, but it is a better place than it was 50 years ago. We have made progress, and we must continue to work towards a better future for all.

On all dates the stage of germination date RLDG was later by 10 to 18 days (Table 3-1). Therefore, on the average, there were no separate estimates of either RLDG or RLSD on a whole plant basis. However, it showed consistently high positive correlations (ranging from .848 to .88) with plant height phenotypes, across populations and years (Table 3-1). Therefore, it was a precise indicator, although not however, indicative of both RLSD and RLDG on a separate phenotype.

The occurrence of 10 reward days prior to RLSD on different genotypes, contrasts markedly with the timing of 100 or 1000 days in late-flowering plants. In the latter, 10 reward days lie at the end of a sequential period of about three weeks during which there is a diffuse plant growth initiation and growth occurs and maturity (PM). Thus an average plant indicator of the physiological maturation of height and growth. The flowering plants remain to be determined.

Flowering date, Rd, of linear plant growth, RLSD, of linear bolting plants, and RL

In most references, the flowering period RLDG on average did not occur 10 days before RLSD (Table 3-1). These differences were significant, except among the genotypes that showed a break in the 10-0-0-0. The result does not serve that usually occurs because maturity probably occurred in an extended period of 10-11 days.

In all cases, positive correlations were found between ILDQ and ILAQ score quintiles. Within experiments (Table 2), in all the experiments were not statistically significant across quintiles. This lack of consistency may be due to differences in the genetic background of the genotypes tested, or to environmental factors, because in 1992 the genotypes in the two populations were planted at different field capacities (from 80-8-0-8 and 10-0-0-8).

In the set of three experiments, entries were in a range (Table 2a), and 37, were ranked almost identically. These 37 entries (entries 100-1000) overlapped (Table 2a). The genotype cross (Table 2) between 1992 were exceptional. They reached 8000 an average of five days later than 87 and their 10 confidence intervals did not overlap. This was the only case in which this showed a weak positive association with 10 entries (Table 2a). In the other two experiments, the positive associations are significant or highly significant (Table 2a). Contrary to the findings of Tieling et al. (1991), these associations results and associations suggest that 10-18-80 always an accurate visual indicator of physiological maturity in rapese plants. The inconsistency may be expected, because the stage of 10 has important gene phenotypic effects prior according to Stigge and Czerny (1991), and because this may be dependent among quantitative genetic values.

Plants reached E2E levels 40-50 days after they reached ET (Table 3.1). Positive associations between mean tree stages were not consistently significant across experiments (Table 3.2). This also occurred near ET, and the time between ET and E2E was not consistent across genotypes and environments.

Correlations among attributes: E2E and EPO, Replications

In two of the three experiments EPP of genotypes from both series averaged about 4 units shorter (P₁₄₋₄₅ and PPO) (Table 3.3). In the other experiment, the average lengths of EPP and EPO were not significantly different, probably due to the lack of differences observed between E2E and E2E1 (Table 3.4). Replication differences for EPP within series were found only among the genotypes in P₁₄₋₄₅-C-18. In all cases, EPO and EPP exhibited highly positive linear correlations among genotypes, with one exception, except for PPO which was not so clear together.

Relationships between EPP and EPO were positive within experiments (Table 3.4), but varied across experiments. Larger PPO's had negative linear relationships between EPP and EPO, which probably due to differences between EPO and E2E1, because E2E2 and E2E1 occurred simultaneously on different life stages. In all cases, EPP and EPO began simultaneously but EPO finished at different times after EPP.

1. *Journal of the American Statistical Association*, 1937, 32, 209-216.

Table 6.2.4. Multidigitized annual average contributions (p) among
Ex-Presidents during Period 1 (1970-1989), Period 2 (1990-1999)
Period 3 (2000-2009). (All, M, F)

	NET M	NET F	EXP M
	EXP F	EXP M+F	EXP F+M
1970			
Presidente a. Repubblica (N=11)	0,10**	0,25	0,32**
Presidente a. Repubblica (N=40)	-	-	0,48**
Presidente a. PES-PSDI (N=10)	0,19	0,19*	0,34
Presidente a. PSDI-PSDI (N=61)	-	-	0,37**
1980			
BORG-Carriera Giovanni a. Repubblica (N=25)	0,49**	0,38**	0,45
1990			
2000			
2000-2009			

*,**: significative differenze tra 2000-09 e 2000-99, con la
t-test di Student.

Visual estimates of the length of seed filling BB-87 averaged eight to 10 days longer (P<0.01) than BPP (Table 3-1). The period BB-87 was also significantly longer than BPP, however, for genotypes from Brazil or Mexico (P<0.01). Therefore, BB-87 was not an adequate estimator of either BPP or BPP_o; minimum sections determined plants reached an overall stage before they received BB-87 or BPP_o, and the timing of BPP, BPP_o and BB were usually different.

Correlations of BPP_o with both BPP and BPP_o showed relationships with strong positive, but the magnitude of associations were less consistent across environments. Therefore, the visual estimate of the length of seed filling BB-87 was not a consistent estimator of previous estimates of either BPP or BPP within environments.

Comparative Stability of Effective Filling Period Estimates Across Environments, 1987-1989

The linear estimates of the lengths of seed filling, BPP, BPP_o, and BB-87, exhibited highly significant genotype by environment interactions among the six genotypes from Brazil or Mexico that were evaluated across 1988 and 1989 (Table 3-2). Therefore, 18 lines of stability across environments. It appears that neither BPP nor BB-87 showed any advantage over BPP. BPP_o and Legg et al. (1973) reported that BPP was least stable across environments, and for that reason they suggested the methods as a selection criterion.

Table 3.3 Mean responses from nine analyses of variance conducted across 1992 and 1993, the extensive training regime (ETR), the representative forced variation (RFV), and RTR-ET and their respective 21 genotypes and their parent numbers and P-values.

Source of Variation	D.F.	FTR	RFV	RTR-ET
Environment	1	53.43	107.55	11.34
Block (Env.)	2	13.49	24.81	2.09
Genotype	9	19.45	42.81	16.20
Gen. x Env.	9	24.87**	51.37**	15.30**
Error	35	5.01	11.36	1.78
CV		2.24%	3.89%	0.41%

*P<0.05; **P<0.01.

Similar results were obtained with the resistance of RS-87 and RPD were measured among larger numbers of genotypes, within populations (Table 2.6). Highly significant genotype by environment interactions were detected for RS-87 in both crosses, and for RPD in one cross.

To further test if the visual estimate of the length of seed filling (RS-87) or genotype (RPD) can interact with environment, different comparisons across experiments were done. In all cases, highly significant genotype by environment interactions effects for RS-87 were detected (Table 2.7). The visual visual estimates for RS-87 was consistently low as the CV values show.

Based-Pearl Irradiation at Different Filling Period, Different Spacing, Yield (%)

The estimate of basal seed heritability for RPD was 28.2%, and for RPD and RS-87 were 3 among six genotypes from crossed *S. Ruttan*. Additional estimates of basal gene heritability for RPD were 3 among 11 genotypes from crossed *S. Ruttan* and 31.3% among 19 genotypes from crossed *S. Pico*-87. Additional estimates of basal gene heritability for RS-87 were also approached around three and crossed (Table 3.6). In the case of crossed *S. Ruttan*, the basal gene heritabilities for RS-87 and yield were similar, but they were inconsistent in the other cases. These results suggest that the set of RS-87 physiological very and RPD

Table 1. A multi-dimensional framework for evaluating the quality of information systems.

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...and the first time I saw it, I thought it was a great idea. I thought it was a great idea because it was a great idea.

Table 3.4. Root mass heritability at week 5(%) and plant height genotypes from two crosses across different environments.

Environment	n	mean	SE(%)
Root length (mm)			
13-0-0-0-0 vs 13-0-1	8	34.4	10.8
13-0-0-0-0 vs 13-0-0-1	11	33.6	11.3
13-0-0-0-0 vs 13-0-0-1	10	-	11.4
13-0-0-0-0 vs 13-0-0-1	13	33.8	11.0
13-0-0-0-0 vs 13-0-0-0	10	43.7	10.4
13-0-0-0-0 vs 13-0-0-0	10	-	11.2

or visual estimates of the length of seed filling, an objective criteria should be quantified among measurements in order to be effective.

Suggestions

The reliability of ET estimates using several developmental protein prototypes from two sources has questions. Consequently, the concept of SPPC, the sum of linear ET increases (estimated allometrically) taken between day 100 and day 150, may have widespread application for greenhouse hybrids, their results allow for a potentially useful and physiologically sound characterization of the length of seed filling. Reproducible Period Duration data, the ratio of final ET to SPPC, is an estimate of the length of the period of linear ET increase such that SPPC is an estimate of the duration of linear seed growth.

Estimates of SPPC and PPD on a whole plant basis obtained from only one early and one late sampling date were equivalent to estimates obtained from sequential samplings performed throughout seed filling. Reproducible Period Duration and SPPC was relatively low (7%) once calculated, independently from SPPC and PPD obtained from three samplings.

In all cases, mean SPPC and PPD increased simultaneously as developmental prototypes from two sources plants decreased in 10 to 15 days before either SPPC or PPD had a significant value. These three stages were positive and

from 1980-81), although it was an incomplete mixture of RPP and RBT or intermediate percentages. It was an adequately positive predictive mixture.

Plots treated with RBT three to six days after were 83% to 90% genotype-RPP treatment seedlings, in two of three cases, differences each significant. RBT is associated with RPP in two of three experiments.

The physiological estimates of the length of seed dilution (RPP and RBT) were positively associated but varied in degree of association. They started at the same time, but RBT dilated up to one week after RPP.

The packed RBT was 8 to 12 days longer than RPP, and slightly longer than RPT. The visual estimate of the length of seed dilution RBT-RPT, was not a consistent, positive, and accurate estimate of either RPP or RPT.

Estimates of broad bean germination for RPP, RPT, and RBT were inaccurate. They were similar, and sometimes lower, than the plots. Therefore, the use of RPP, RPT or RBT as inoculum criteria in mybean breeding, appears to be somewhat dubious. Also, selection for longer seed dilution periods would have to be prioritized before any improvements in variety to be effective.

CHAPTER 19
ASSOCIATION BETWEEN FIELD AND FILLING PERIOD ESTIMATES
ACROSS STERILIZED AND FRESH SEED CULTIVARS

Introduction

Ramsey and Baker (1975a) found that seed yield was more a function of the length of seed development than of the date of seed growth in a field area trials, among eight barley genotypes. Bell and Zuppan (1973) found a positive relationship between Effective Filling Period (EFP) and seed yield of two genotypes. Based on similar results, Day et al. (1980) suggested that yield improvements in the future may be possible by lengthening the filling period. However, the use of estimates of the length of seed filling in breeding programs to intentionally select for higher yielding varieties has not been reported.

Initial estimates of the length of seed filling are easily determined. Probably for this reason reports on EFP estimation with plant life often found in the literature, especially after Bell and Zuppan (1973) described specific developmental stages. The period between observed cumulative percentage anthesis and 50% seed filling (Barley maturity criterion in different environments) (Bunting et al., 1979), DeWet (1973) found a strong significant positive association between EFP and yield of eight

Intersubjective genotypes. Rane (1981) reported a positive correlation between 35-38 and yield of several entry-grown genotypes from different maturity classes. However, in three out of four experiments, yield losses in plants of the longer fallowing periods relative to the control of the length of seed fallowing amounted to variability 127±0.52% at 0.05% and were positively associated (ranging from yield among genotypes with different seed position variants (Bentley, Rane and Rane, 1981).

In studies where positive associations between yield and different measures of the length of seed fallowing were found, associations were not consistently strong. Willis, Daugay et al. (1971) found that the parent itself was the most highly correlated with yield among numerous genotypes; the correlation coefficients ranged from 0.29 to 0.54 across varieties and stages (1971). Daudet (1975) found that only about 10 % of the yield differences were explained by differences in sowing techniques or the length of seed fallowing.

In the studies cited, associations between yield and different measures of the length of seed fallowing were determined on selected genotypes with no attempt made to select for high yield, i.e., different varieties. In order to adequately represent yields within populations used by farmers, associations between yield and the length of seed fallowing should be determined on representative samples of local genotypes in their diversity.

However, it is likely inferred that correlations between PGR-100, PGR-100 and negligible (<0.01), and PGR-100, PGR-100 and PGR-100 were due to groups of similar soybean genotypes. If these effects were confirmed among further genotypes in other genetic backgrounds, inherent selection for plants using substances of the Design 100 and PGR-100 would be questionable in soybean breeding.

The approach of the association between plant and the Design 100 and PGR-100 seems important, however, even though the selection of genotype by experiment component associated to stages (II-III) shows considerable applications. Obviously, seed pitch is a measure of the rate of seedling weight accumulation in a land area basis (SOP), and of the duration of this process.

Another approach to study the dynamic relationships of factors in plant growth, including sow and duration, is the use of simulation models empirically developed for maize response under CIMA (Pereira de Vries and van Laar, 1991). Several simulation models have been developed with different purposes for pasture and cover crops (Rabey, 1993); however, up to now we apply, or have been developing, or study crop management simulations, a simple simulation model that incorporates the concept of the rate of dry matter addition over time since we concentrated the primary purpose of the model was to generate hypothesis from some indications in soybean breeding, rather than trying to mimic soybean growth. An

symmetric association of the yield and seed size that appears prior to seed growth limit neither yields nor the seeds that regenerate day earlier restrict the production and development of seeds.

The use of a stochastic model would allow the examination of the type and strength of the association between yield and the length of seed fallow, and also would support additional parametric results which may influence the nature and strength of this relationship.

A dual approach was taken to examine the relationship between yield and seed falling duration to daylength. First, a simulation model of soybean reproductive growth was developed, and a simulated set of soybean genotypes was generated through sensitivity analysis of the model. The set of simulated genotypes was assumed to be representative of a population of soybean genotypes. Relationships about the type and strength of the association between yield, RPP, and RPI were developed using the simulated genotypes. Second, two linear hypotheses were field tested using random genotypes (2008 test series) in 2008 year, and in another year, genotypes used were selected to represent differences in yield and seed falling period duration. Additional objectives were to determine the nature and strength of the relationship between yield and RPP values and across environments, using two-stage analysis.

Model and Methods

Model Development

This model was developed to examine the association among different weather and physiological processes and their relationship with yield, in order to verify hypotheses that have potential implications in developing higher-yielding systems. The model was intended to simulate systems reproduction growth under non-controlled environmental conditions, which were assumed uniform throughout the simulation period. The use rate of potential water per season available for crop production (PRAF), were simulated under constant throughput need setting. We used PRAF's of 100, 100 and 300 mm/a day of income. The last two values correspond to the average values reported by SINGH and DE JAE (1979).

The model simulates soybean crop growth from the beginning of linear to late reproductive (determinate flower leaves) until maturity. It was assumed that effects prior to that period influence primarily the amount of reproductive biomass at the beginning of seed growth (DEB). And that the later ones affect (LAI) and excess of seed area. For that reason PRAF is used as a static input; values for DEB used in the simulations were between 2100 and 2700 kg DC dry weight/ha, which correspond to values cited by BENNETT (1977), and SINGH (1979).

It was assumed that leaf litter accounts for 20% of basal, the rest being branches and stems. Leaf area index (LAI) was calculated as the ratio of total dry weight converted leaf weight. An average specific leaf weight of 0.6 g dry weight⁻² of leaf area was used to estimate leaf conversion leaf weight.

The ash-free combustion efficiencies defined by Prentiss et al. (1978) to produce ash-free pyritic, pyritic humic material or the nitrogen mineralized basal, and lignite from biomass were used to calculate biomass protection and protective biomass and ash. It was assumed that prentiss has 90% N and C0₂ contents of 0.16 (ash-free) and 0.05 (ashed) as done from Bond et al. (1978). Pyritic and ash were assumed to have 2.0 and 1.00 N, respectively, based on data by Ramsey and Rasmussen (1971). 4) Biomass loaded from estimates of tree symbiotic nitrogen fixation were not distinguished, because the lower efficiencies tree symbiotic nitrogen and volatile according to Sherry and Rasmussen (1971). Seeds were assumed to have a constant composition hexopyrone and protein as reported by Gallois, Rasmussen (1982). Seed composition was set to 40% protein, 30% lipids, 20% carbohydrates, 4% lignin, and 1% ash. Out these ratios would be changed to complete the addition of seed composition to other roots and stemwood. Based on these combustion efficiencies and assumptions, one unit of biomass yields either 0.155 units of volatile dry weight or 0.470 units of root dry weight, the former value was

used by Rensink and de Wit (1991).

Another model input is the pace of an increase/decrease discrepancy (Rötter, 1984), as defined by Schmid-Burgess et al. (1994), which is evaluated between Christopher and Wilcox, the range is 0.001 and 0.01 between 0.001 and 0.005 day⁻¹ because similar values were reported by these authors on some quantifiers under good growing conditions.

Model description

A single model version in BASIC was developed to account for the dynamic balance of carbon and nitrogen during soybean seed growth on an energy maximizer basis (Oppenhuizen, 1971). Because the interpretation is performed in opposite each time variable with a time interval of 0.2 day, and the model outputs the state of the system on a daily basis with the values of each variable expressed in kg/ha. The initial inputs to the model are PGRD, PGRD, and PGRD. The values of the initial inputs used in the sensitivity analyses are presented in Table 4 and

The first step in the flow diagram of the system (Fig. 4.1) is to calculate the daily rate of net losses production of the crop (RGRD) which is available 200 hours synthesis after respiration; in this case the empirical formula based on PGRD and LRD derived by Rensink and de Wit (1991) was used to calculate RGRD. Net production is

Table 4.1. Input variables for sensitivity analysis of the simulation model of nitrogen reproduction growth.

Variable	Range	Values tested
Initial N supply (kg/ha)	0-1000	3000, 1000, 3000
Potential biomass net biomass production (kg/ha)	0-10000	1000, 1000, 1000
Rep number allocation coeff (0.0001- 1.0000)	0.001 ^a	0.011, 0.011, 0.011, 0.014, 0.018

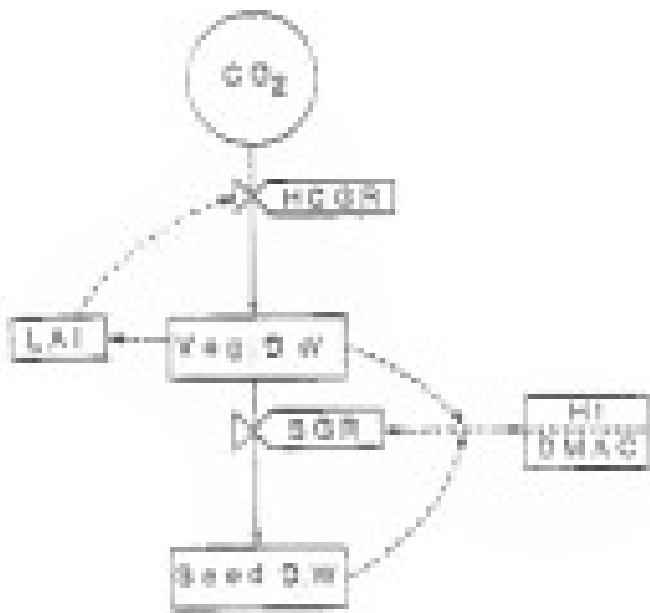


Figure 4-1 Flow diagram of the model of soybean reproduction process.

transformed into vegetative biomass using energy equivalent values to form a vegetative dry matter pool.

Total seed growth rate (RSD) on a dry weight basis (kg/m² x day) is estimated through successive iterations, as a function of the current plant dry weight and RSD, a post-harvested reduction factor for a RSD value that allows RSD to remain constant, within a given error tolerance. The reduction pattern of seed dry weight accumulation follows a logistic curve with a long linear phase. An assay proportional to RSD on an energy equivalent basis is also determined from the vegetative dry weight pool. This factor allows the simulation of the effect of different composition of vegetative stages as well as seed on other stages and processes by simply changing the energy equivalent ratios.

For this RSD to result that RSD on an energy equivalent basis, the vegetative dry weight pool is addressed accordingly. It was assumed that a negligible amount of seed grows from plant dry weight after RSD growth. Therefore, biomass in the vegetative dry weight pool (LR day) during seed filling, increases with dry weight.

Ratio LRW to LRSD greater than 0.95 on an energy equivalent basis is optimum, since it is a net loss of vegetative materials through translocation or utilization by seeds. To account for the loss of material from vegetative stages, the total dry weight proportion (LRW)

increments of 20% gas, nitrogen, and water as the basis of the energy equivalent value of these three degrees of the R factor used by the "DRC-Standard" model by Gosselink and de Boer (1979).

It was assumed that initial dry weight decline averages for about 60% of the vegetative dry weight decline that occurs during seed filling. In terms of total energy equivalent units, the plant percentage losses are indicated the seedlings translocated to seeds, as well as the portion that is irreversibly lost as fallen leaves that were assumed to be 20% of the total dry weight decline. These percentages are based on the higher nitrogen content of seedlings compared with pasture and grass (Kinney and Weber, 1972) so, total seedling dry weight loss amounts for approximately half of the vegetative dry weight loss during seed filling (Kinney and Weber, 1972).

Simulations are allowed to proceed until the available DRC is totally depleted; at that point it is assumed that herbivory has been removed. The model then computes the final status of the system. The duration of seed filling, determined by the model, is representative Period Duration (PD) = Effective Filling Period can be calculated, then, as the ratio of Final seed weight to the rate observed during the linear portion of seed growth.

A total of 45 simulated response prototypes were generated through sensitivity analysis of the simulation model with respect to production growth, as low as 10%

values presented in Table 4.1. Data on the different genotypes were fitted to a linear regression model to examine the type and strength of the association among seedling diameter reduction, mean physiological traits, and yield.

Field Experiments

The hypotheses regarding how the simulations were distributed using paired data from 16 experiments. The results and details for all of them were described in Chapters II and III. Thus, the more agriculturally important processes will be described.

Yield data from the experiments performed at the Agricultural Research and Education Center, Quincy, Florida, and Gainesville, Florida in 1980 and 1981, and at Citrus Research Park near Gainesville, Florida in 1982 were used. Irrigation data for field and citrus trials, detailed in Table 4.2, from five other experiments performed at Gainesville, Florida in 1980 and 1981 were also used. Irrigation was used to supplement rainfall in only one case (Table 4.3(a)).

Table 4-10. Test factors measured in the experiments at Göttingen (in: PROGAR, 1970) and (198).

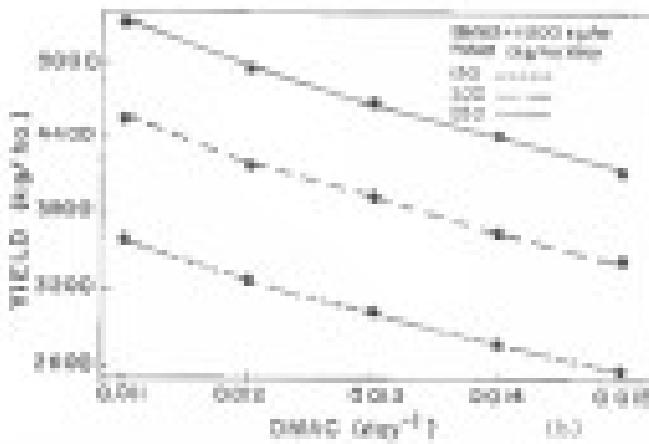
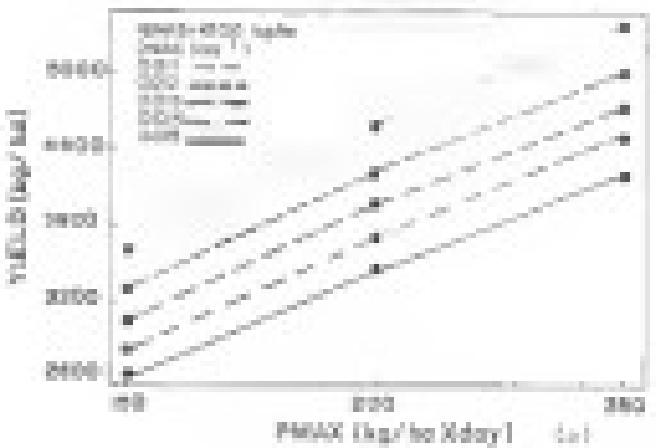
TEST	Number of Countypes	TESTS
R1-R-1-R	8	EPF, EPO, R1-R1, Yield
R1-n(R)-R	10	EPF, R1-R1, Yield
R1-R-1-R'	8	EPF, EPO, R1-R1, Yield
R1-R-R-R'	10	EPO, R1-R1, Yield
R1-R-R	10	R1-R1, Yield
R1-R-R	10	EPF, EPO, R1-R1, Yield
R1-R-R	80	R1-R1

Results and Discussion

Model factor analysis of T₄₅₀ as a function of the model inputs

To examine the dependence of yield on model inputs (DMRD, PGR4, and DMRC), a simple factor analysis was performed using simulated parameters. By doing so, it is possible to determine the dependence of yield on one input at a time, while the others are held constant (Fig. 4-2-1). At a given PGR4 level (0.00 ppm), yield shows a nearly linear increase with PGR4 concentration, and higher yields correspond to the lower DMRC values (Fig. 4-2-1a). Yield increases with increases in PGR4, and the higher yields correspond to the higher PGR4 levels (Fig. 4-2-1b). Similarly, at a given PGR4 level (0.00 ppm), yield increases with DMRD, and higher yields correspond to lower DMRC values (Fig. 4-2-1c). While yield decreases with DMRD and higher yields correspond to higher DMRD levels. Finally, at a given low PGR4 (0.003 ppm), yield increases with increases in either DMRD or PGR4 levels (Figs. 4-2-1a and 4-2-1b).

The above results will be used in formulating recommendations to farmers to obtain yield through breeding (Chapter V).



FIGURES 1, 2, 3. Yield yield as a function of Temperature. Results with known production rate (DMAC) of 0.04 days⁻¹ and dry weight allocation coefficient (DWAC) of 0.05, with a constant shoot:root ratio (0.6667), in simulated maize crop ecosystems.

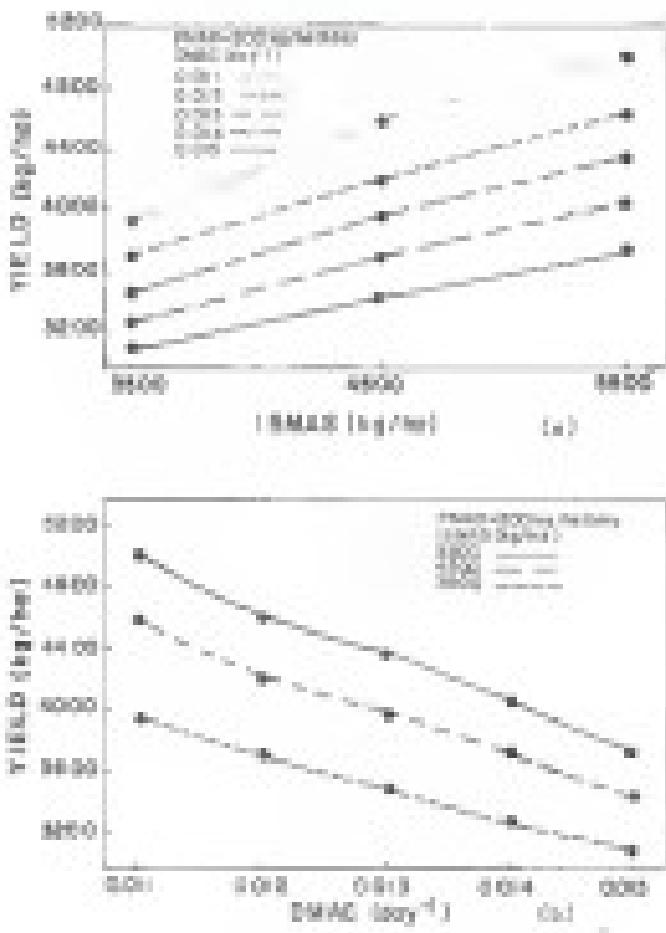


FIGURE 8.7.3 Yield (kg/ha) as a Function of DMAC (kg/ha) and Seed Rates (kg/ha) for Various Concentrations (kg/ha) of DMAC at a constant $R_{DMAC} = 0.1$, $R_{SEED} = 0.1$, $R_{POTATO} = 0.0001$, $R_{FERTILIZER} = 0.0001$.

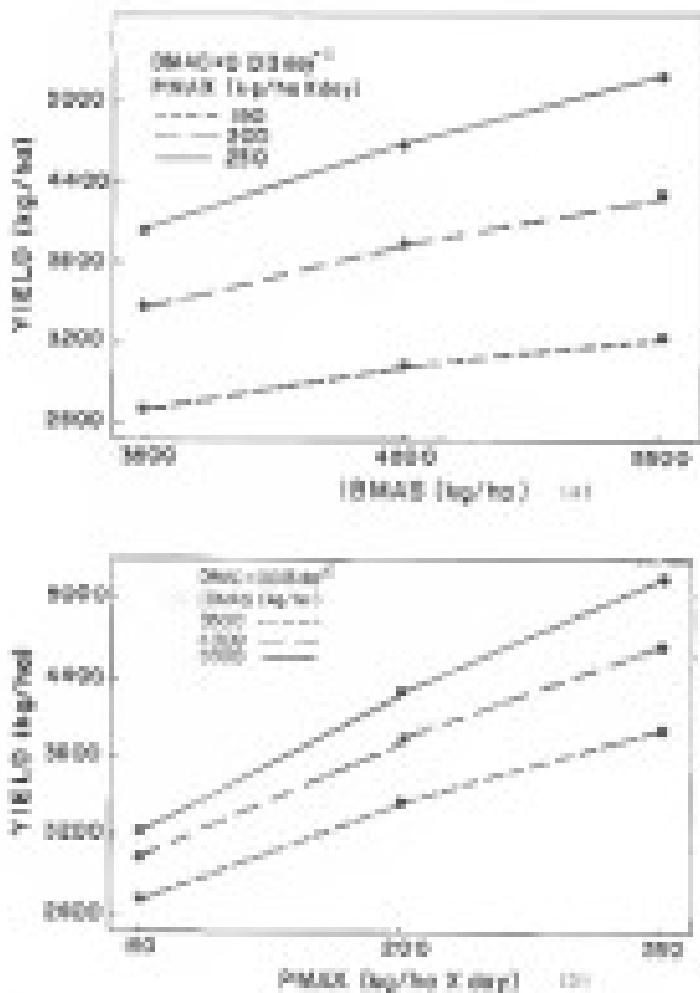


Figure 4-2-2. Yield yield in a function of different biomass increase in GAI, and different biomass increase reduction (PGR) in 100, 200, and 300 days after 2nd till (GAI = Green Area Index) (PGR = plant growth regulators).

Relationship between yield and growth of seedlings of different genotypes

A positive association between yield and RPP was predicted from 45 simulated soybean genotypes, and 32% of these yield variations were explained by the variation in RPP (Fig. 4.3). Field results show that similar patterns of the yield variation in our field experiments are explained by the variation in RPP (Figs. 4.4, 4.5, and 4.6). In all cases, these associations were not significant. The range in RPP among the genotypes is very slender and narrow (1, to 21 days), and genotype differences for RPP are non-significant. Thus, it is not surprising that the association of yield with RPP (Fig. 4.7) was also non-significant.

A positive association between yield and RPP was predicted by the 45 simulated soybean genotypes, but the linear regression of yield as a function of RPP explained only 40–100% of the yield differences (Fig. 4.7). Results from the years of field experiments with 17 Chinese genotypes from two sources support the hypothesis formulated with the simulation model (Figs. 4.8, 4.9, and 4.10). In 1982 twelve genotypes were used by our first hypothesis, while in 1983, genotypes were divided in different differences in yield and seed filling duration. In all cases, linear regression of yield as a function of RPP explained similarly a small portion of the yield differences.

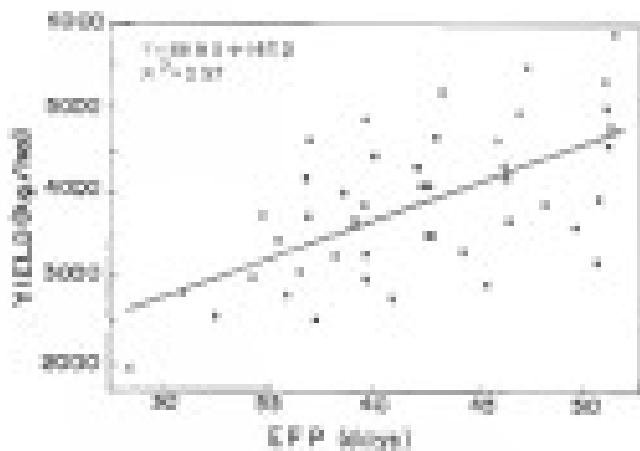


Figure 4.2.3. Yield yield as a Function of Effective Tillage (derived from 1999-2000 simulated experiments).

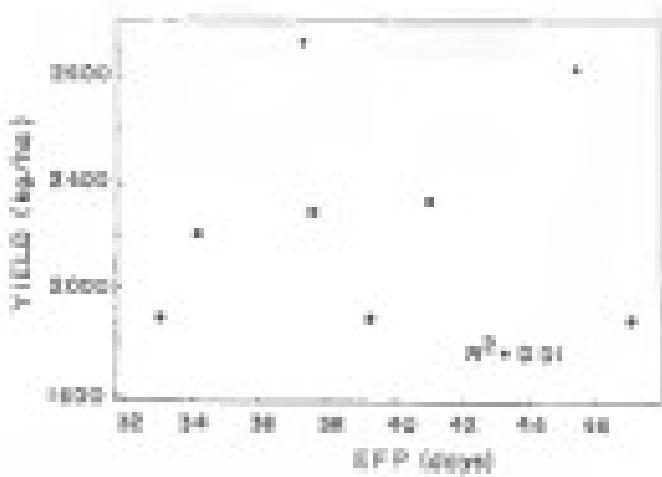


Figure 4.6: Data points as a function of EFP (days). Fitting period: 1971-1992; $n=16$; $R^2=0.31$. PT response genotypes: 0 non-flowering or flowering in first 30 days ($n=8$).

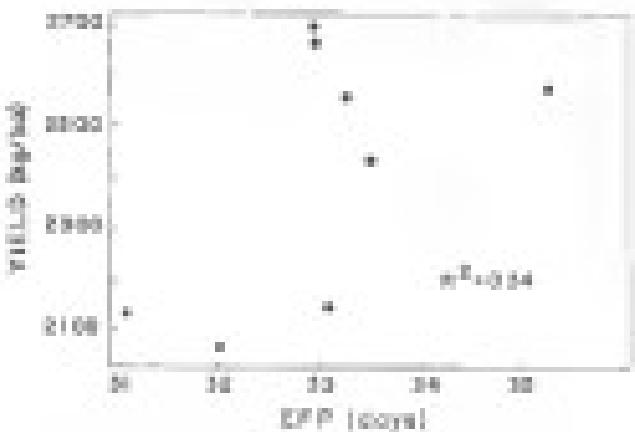


Figure 4.3. Seed yield as a function of different EFP (days). Points obtained from different P2 progenies (n=4). From Deneffe et al. (1991).

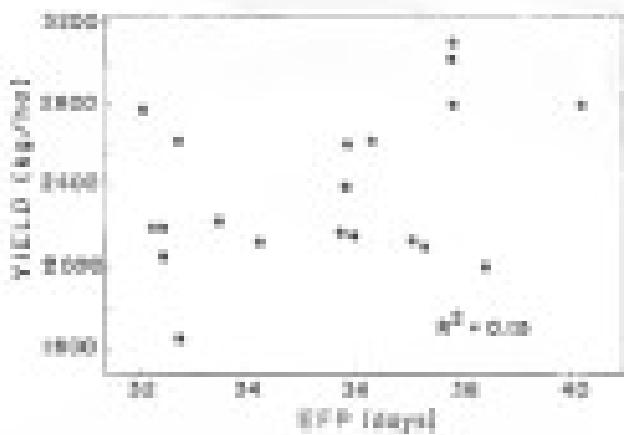


FIGURE 4.26 Seed yield as a function of different PEP (long duration, LDP), being measured PEP expression genotypes from barley in barley and wheat a DLS-MLL, i.e. DLSR 81-0-1.

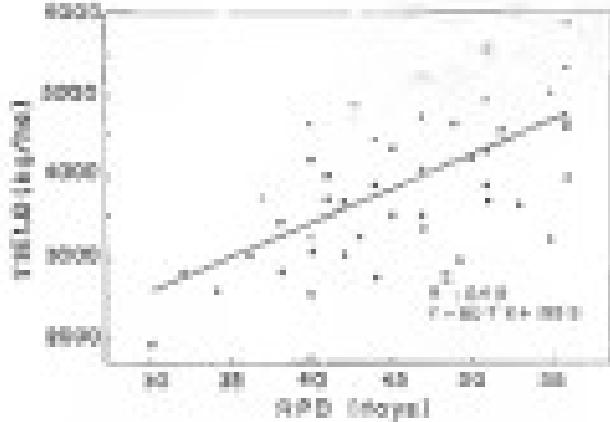


Figure 4. Yield yield as a function of supplementary
Teffid Granules (kg/ha), under different
cultural practices.

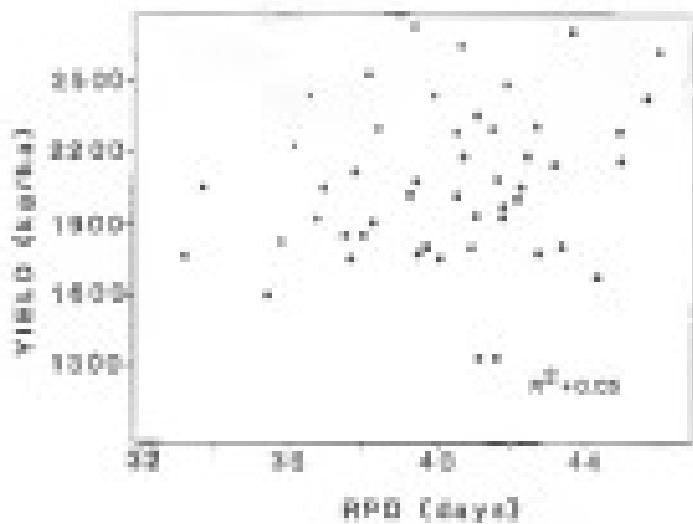


Figure 4.5. Yield yield as a function of the post-harvest Period Duration (RPD), using random P7 selection quantiles from logistic regression on Test data set.

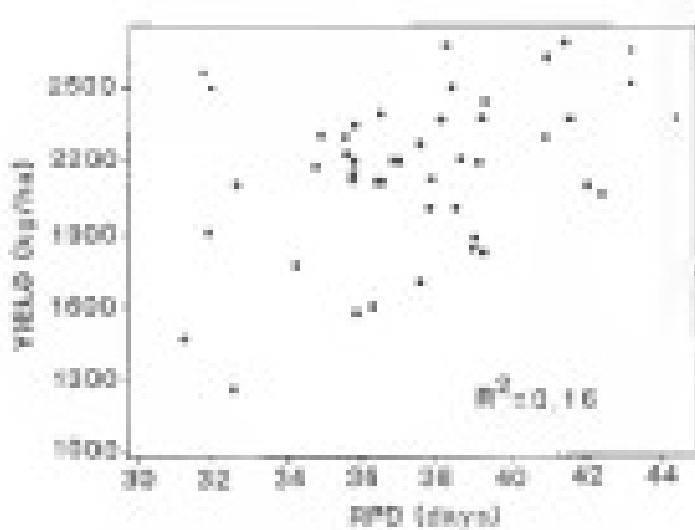


Figure 4.10. Seed yield as a function of Reproductive Period duration (RPD), among eleven F3 soybean genotypes from Brazil x PIS-0100 in plot 31-6-3-4.

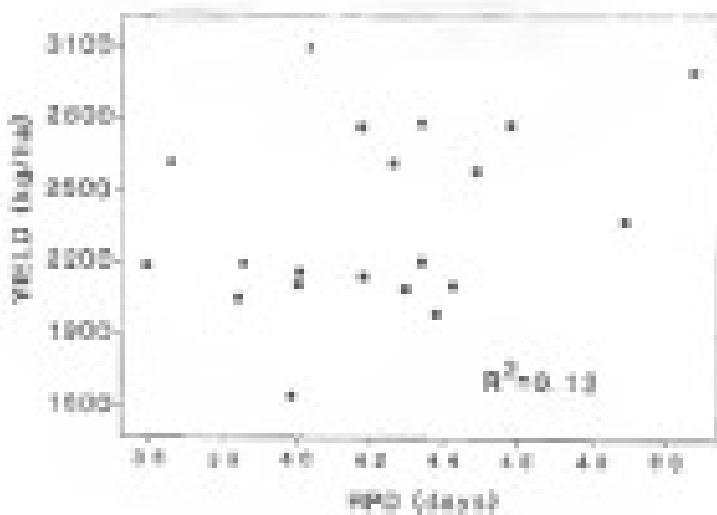


FIGURE 4-18 Seed yield as a function of reproductive period duration (PPO), among 73 soybean genotypes from Brazil's EMBRAPA and Instituto de Pesquisas da Terra (IPT).

The relationship between yield and 85-87 recorded additional evidence for weak positive associations between yield and the length of seed filling period among mutant genotypes. In 1982, the linear regression of yield as a function of 85-87 mean number quinques from two crosses predicted a small portion of the yield differences (Fig. 4.11 and 4.12). The slopes of the predicted lines were not significantly different than zero. Similar results were observed in 1983, when the genotypes studied were subject to different yield and seed filling differences. Although in those cases the associations between yield and 85-87 were highly significant, only about 40% of the yield variation was explained by the linear regression model (Fig. 4.13 and 4.14). In all three genotypes with high and low yields were found when the periods 85-87 were longer. Therefore, selection for long 85-87 would not have necessarily implied selection for higher yields.

Since yield is a function of SDR and the duration of seed filling, these results indirectly support that SDR may be more important than the length of seed filling in determining the yielding ability of certain genotypes.

Differences in length of seed filling between seed yield and the quality of seed filling within experiments

In order to measure which factors influenced the weak positive relationships between yield and differences in expected SDR and filling duration observed within experiments, the

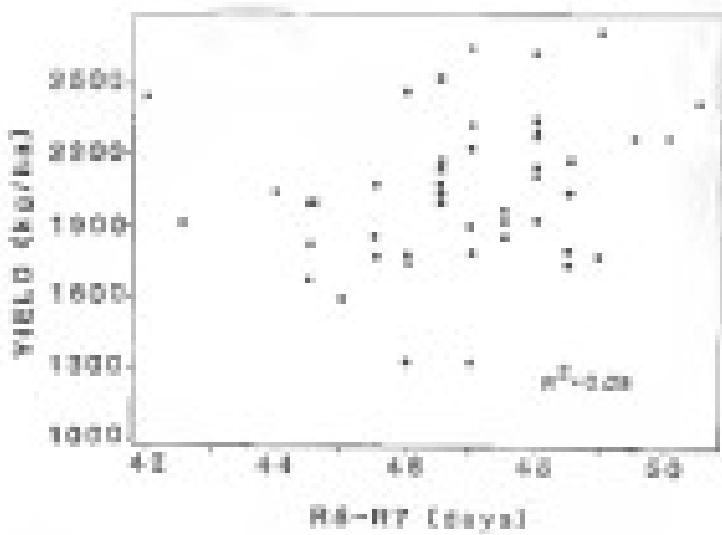


Figure 4.11. Yield field as a function of the period R4-R7 among random 17 soybean genotypes from Brazil. $R^2=0.68$.

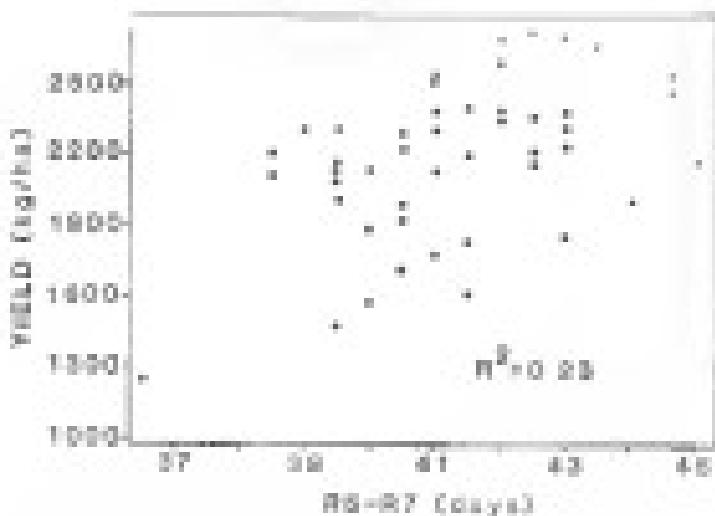


Figure 4.12 Feed price as a function of the period RG-R7 among centers of soybean groups from November 1994 to April 1995

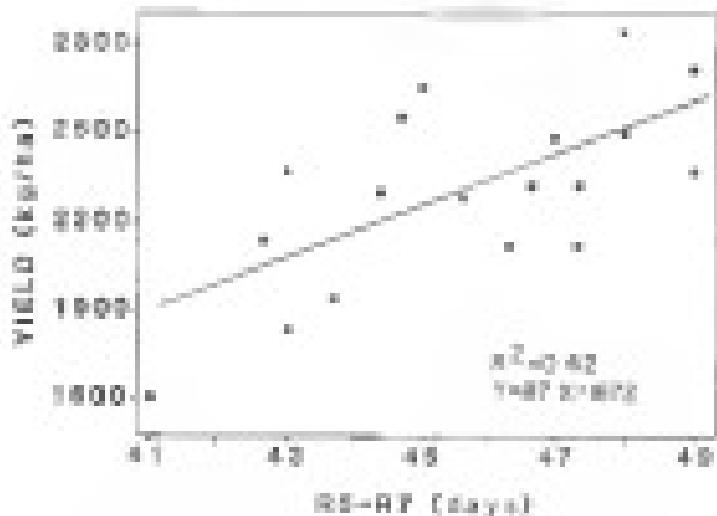


FIGURE 4.13. Yield plotted as a function of the period RGR-RF among 22 soybean genotypes (1998). Regression equation and statistics: $y = 171 + 10.4x$, $R^2 = 0.42$, $P = 0.072$.

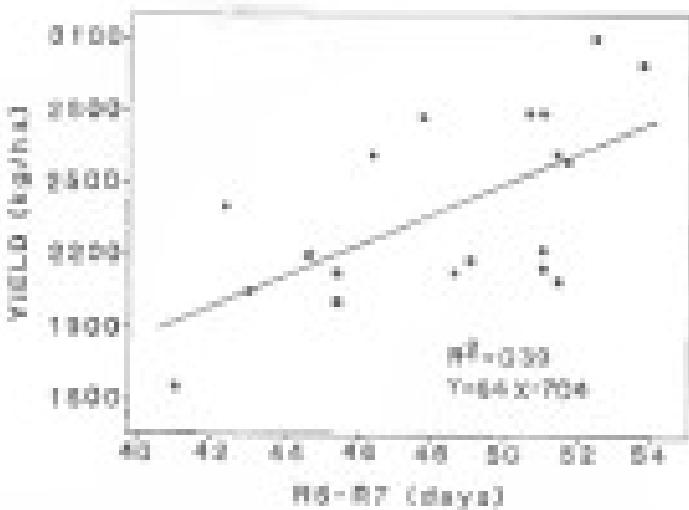


Figure 1.1.1. Seed yield as a function of the period P5-P7 among 17 different genotypes from Mexico to Mexico and Brazil x 194-195-197-198-199.

characterization of simulated genotypes were included in a plot of yield versus EPP (Fig. 4-15). In this case only 18 simulated genotypes were used for demonstration purposes. The highest yield corresponded to the simulated genotype with lowest EPP, highest DMG and PGR levels, and lowest DGR.

The Dry Matter Allocation component exhibited strong and weak negative influences, respectively, on the length of EPP and yield among simulated genotypes (Fig. 4-16). Field results showed close agreement with the simulations. In all cases, negative correlations were highly significant between EPP and cutting period biomass and nonsignificant between EPP and yield. A detailed analysis of field data on this subject is presented in Chapter VI.

Within a given DGR level, increasing in DMG and PGR produced sharp yield increases, but EPP remained essentially constant among simulated genotypes (Fig. 4-17). Field results from one year support this hypothesis (Chapter VI). Therefore, the weak positive associations of yield with EPP and other estimates of the length of post cutting observed among simulated and field genotypes ungrouped within environments were probably caused by the differential influences of DMG, PGR, and DGR on yield and EPP.

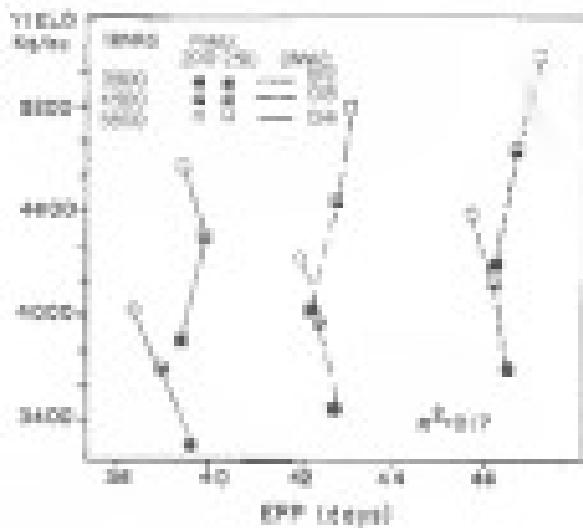


Figure 1-11 - Effects of increasing fiber content on TIELO, shear yield and stiffness. Full-line symbols denote calculated quantities.

Regression analysis field and length of joint falling
SEEDS/HECTARE

The associations between yield and DPP were non-significant and low correlations across environments (Table 4.1). Yield in 1993 was positively correlated with DPP estimated in 1992, but yield in 1992 was negatively correlated with DPP estimated in 1993. Thus, DPP was a poor predictor of yield across environments as it was within environments.

Similarly, the associations between yield and the mean seedlings/hectare across years and environments (Table 4.1). Therefore, DPP was a poor predictor of yield within as well as within environments.

The lack of dependency of DPP estimates across environments (Table 4.2) was supported by the non-significant correlations between DPP estimates across 1992 and 1993 in both environments (Table 4.2). Therefore, yield from each year was a better and more consistent predictor of yield across years than DPP, among the genotypes from both environments.

The associations between yield and P-hat across 1992 and 1993 were either null, or positive and non-significant among the genotypes from both environments (Table 4.3). The only exception was the non-significant negative correlation between P-hat estimated in 1992 and yield in 1993 (Table 4.3).

Estimates of P-hat showed low variability or no dependency between 1992 and 1993 among the genotypes from DPP studies (Table 4.3). These results were probably due

Table 4.3. Phenotypic correlations (r) between yield traits and relative yield period (RYP) across 1982 and 1983, among all selected F7 wheat genotypes from the same breeding program

Variable	1982 Yield	1983 Yield	1982 RYP
1982 RYP	-0.10	0.10	-0.10
1982 Yield	-	0.33	-0.43
1983 Yield	-	-	0.45

Table 4-4. Phenotypic correlation coefficients (r_p) between mean yield and reproductive period (yields 1981, 1982, 1983 and 1984), among selected 37 soybean genotypes from the dataset.

GENOTYPE	1981 MEAN	1982 MEAN	1983 MEAN
Bontida x Mariana (var.)			
1981 BPP	0.854	0.13	0.03
1981 T2610	--	0.13	-0.11
Bontida x PGI-120 (var.)			
1982 BPP	0.108	-0.07	0.10
1982 T2610	--	-0.100	0.19

* Significant at 99.9%.

TABLE 6.5. Phosphate concentration differences (μM) between 1970 and 1987 versus 1987 and 1991 among 17 samples grouped from two criteria.

TREATMENT	1970		1987		
	$\text{P}_{\text{NO}_3+\text{PO}_4}$	P_{NO_3}	$\text{P}_{\text{NO}_3+\text{PO}_4}$	P_{NO_3}	P_{PO_4}
Benthic \rightarrow Benthic					
1970	-0.14 (n=6)	-0.12 (n=12)	-0.21 (n=10)	-0.17 (n=10)	-0.18 (n=10)
1987	-0.23 (n=1)	-0.15 (n=12)	-0.24 (n=10)	-0.13 (n=10)	-0.21 (n=10)
Benthic \rightarrow POM-POM					
1970	-0.26 (n=10)	-0.19 (n=10)	-0.42 (n=10)	-0.11 (n=10)	-0.24 (n=10)
1987	-0.31 (n=10)	-0.17 (n=10)	-0.35 (n=10)	-0.10 (n=10)	-0.25 (n=10)

* Significant at 0.05.

in the highly significant ($P < 0.01$) genotype by environment interaction for yield difference among the genotypes from both crosses and reported in Chapter III. Yield predictions showed consistent positive associations between LTHD and LTHG within crosses (Table 4.6). Therefore, in general, yields in either 1980 or 1981 were better although not precisely estimates of yield across years than RHT-RT among the genotypes from both crosses.

To test further if RHT-RT could be used as a selection criterion to predict the yield performance across environments among various genotypes, yield data from various experiments performed at Sebringville and Galaxy, Florida in 1980 and 1981 were correlated with RHT-RT estimates for the same variety genotypes at Tallahassee, Florida, in 1980 and 1981. Again, the presence of low negative correlations between field and RHT-RT across environments was observed (Table 4.7). Correlations were either low positive to negative, or essentially away from 1.00 for genotypes from both crosses. Similarly, correlations of average yields across six environments per combination and RHT-RT measured in 1980 and 1981 were, respectively, $r=0.22$ and 0.27 and 0.15 , for the genotypes from variety *A* 1010, and $r=0.23$ \pm 0.18 and 0.16 ± 0.11 for the genotypes from varieties *A* PDS-1010. These results suggest that the use of RHT-RT estimates obtained in any one year to predict yield of major genotypes across years is not feasible. In addition, the estimates of the lengths of seed filling would

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1990 to be associated with an linear increase plateauing around 10 units to be a stable selection criterion to breeding for higher yielding varieties.

Conclusion

Statistical analysis and field experiments, performed with random PR soybean genotypes from one season to the next, showed that weak positive associations can be present between yield and both RPP and RPS within environments. The linear regression model of yield as a function of either RPP or RPS explained small portions of the yield differences among random genotypes within environments. Therefore, selecting for long filling periods (RPP, RPS, and R-RY) did not necessarily imply selecting for higher yields within environments. These results are interpreted to support that yield growth over a long area basis may be a more important genetic objective than filling period duration.

Statistical relations, that were positive associations between yield and physiological measures of seed filling duration (RPP and RPS) can be expected, due to the

differences) between all three, 1982, and 1983, on yield and seed filling therefore, the higher yields were observed in the smallest groups with the longest SFT, highest TBSAS and PMS, and lowest DMS levels.

Correlation and covariation between yield and differences of the filling period (SFT, PMS, and DMS) were observed across cultivars. Therefore, it appears that the prospects of utilizing the length of seed filling as a selection criteria to select for higher yields among breeding lines are rather limited.

CHAPTER IV
ASSOCIATIONS BETWEEN FIELD AND LABOR COSTS BASED ON 19
INSTITUTIONAL, 1980 AND 1989 AREA DATA

Introduction

Plant seed yield is a crop variable from the intersection of a large number of processes that take place throughout the growing cycle. Individual Seed Growth Data (ISGD) is a process that integrates many other processes and contributes to seed yield. Rummel, Bell (1979) found that ISGD estimated during the linear phase of seed growth was not an important yield-determining factor among four soybean cultivars. He found significant differences in 1980 among cultivars, and a negative but non-significant correlation between yield and 1980 Number of seeds per spike. Rummel also correlated with plant height and accessions environments.

Bellier (1970) found that once the linear phase of seed growth had started, ISGD was not affected by short-term environmental stresses which resulted in reduced individual productivity. Duthie and Deppe (1970) showed that seedlings stored in refrigeration tanks acted as buffers to individual poor conditions. ISGD had several uses. These authors reported that the rate of soybean seed growth within environments was described as a large matrix by averaging within the area.

COVARIANCE TESTS may also influence (BRIER, 1971). BRIER reported considerable variation among crop cultivars in 1968 across planting dates. Lower 1968 were observed by BRIER et al. (1971) in various soybean cultivars at a year when lower temperatures were present. Lower temperatures also reduced general plant growth rates under elevated conditions (REEDER et al., 1991). Thus differences in the above measurements should be expected. Further studies should provide information on the influence of genotype by environment interactions for these.

Soybean genotypes with larger seeds exhibited higher 1968, but there were relatively constant mean early and late sown plots (BRIER et al., 1971). In other cultivars, however, late sowing seeds consistently had better root storage and translocation (BRIER, 1971). The timing of 1968 translocation was sequential in plots from different sowing within plants in an individual genotype (REEDER and BRIER, 1991). Therefore, 1968 should be described as a whole plant factor. If translocal translocation between genotypes are to be used,

seed growth rate in a land area basis (BRIER) is substituted with 1968, as the product of 1968 times the number of seeds that are actually germinated per unit area. Furthermore, seed yield results directly from soil and the length of time this process is facilitated by the plant, the relationship between 1968, the process that ultimately leads to seed yield, and plant traits appears to be inconclusive.

in response, their reported genotypes difference in seed yield exhibited similar trend (Ranney and Baker, 1973a). Reproducible differences in SOR were observed in two wheat cultivars which did not exhibit yield differences (Ranney and Baker, 1973). Differences in SOR between two genotypes were observed in one year when yields were similar (Ranney and Baker, 1973). In all these cases the differences were not related to yield differences.

Bennetts (1977) observed a significant ($P < 0.01$) positive correlation between seed yield and the among-wheat genotypes, no columns, SOR, and reported similar observed higher yields in two genotypes in a year when SOR's were lower, the existence of genotype by environment interaction for SOR was also supported by the latter.

Genotypes in the studies cited above usually were compared, highly selected and high yielding cultivar varieties. In order to adequately represent trends within populations (cultivars etc.) the association of yield with both PGRs and SOR should be determined among random genotypes within varieties.

ESTIMATES of SOR are less precise. Carter et al. (1988) reported relatively high SOR's for dry weight ratios in different wheat crop growth analyses. Therefore a more precise means of estimating SOR would be desirable, no detect differences among genotypes among reasonable numbers of replications. It was noted, for example, that SOR calculated on the product of each type one hundred of mature seeds per plant,

While BSR retained in this way was not statistically significant from yield, because seed quality is a yield component, it was the only practical method available at the time to precisely measure BSR.

The analysis presented in Chapter 17 showed that a strong positive pattern of the yield differences among unselected and selected soybean genotypes over the seasons could be attributed to differences in the length of the filling period (estimated as BPF, BPH and MDF). Such results inherently supported the possibility that BSR was a more important yield-determining factor than the length of seed filling.

Information on additional plant characteristics and processes that influence the association of yield with seed quality is critical in understanding the complex associations of farmers from which seed yield results.

The objectives of this work were to examine the associations between seed yield and BSR in selected soybean genotypes, to determine the strength of the association of yield with both BSR and BPH among genotypes from the GSSB under RIRIAC conditions, and to compare the magnitude of genotype by environment interactions for BSR and BPH with that for yield among genotypes from the GSSB. Additional objectives were to examine, mainly with the use of the association model described in Chapter 17, the relationship of various yield influences on the association of yield with seed.

Materials and Methods

A total of 48 numbered soybean genotypes were generated through association analysis of the fluorescence (light) trait of soybean reproductive growth described in Chapter 11. The initial steps of the model tested in the associability analyses were presented in Chapter IV. Trait and PDR values of the selected genotypes were fitted by a linear regression model to generate inferences about the nature and strength of the associations between these two traits.

The resulting hypothesis was then tested using partial data from tests 13-0-1-9, 13-0-1, and 13-0-2. The materials and methods for these tests are described in Chapters II, III, and IV.

The materials used in 1992 were eight different soybean genotypes from each of the following crosses: soybean x soybean (test 13-0-1-9) and soybean x field-cultivated soybean (test 13-0-1-1) described in Chapter II. Because a released variety was used as an additional check in the latter case, a total of 10 genotypes from both sources was tested in test 13-0-2.

Mean 1992 was subjected as described in Chapter III to seed growth rate as a trait and basal PDR was calculated as the product of 1992 times the number of mature seeds per plant, and expressed as kg/m²/day. Total Basal Seed Weight (TSW) was determined using 200 mature seeds from each plot.

Results and discussionEstimated and total grain yield, grain quality, and yield
differentiation of wheat genotypes

In all cases, the SE's for 1981 were higher than the SE's for either 1980 or yield grain (Tables 3.1 and 3.2). Nevertheless, the SE's for 1980 and 1981 were considerably lower than the ones reported by Carter et al. (1981) for several dry weight traits. Thus, in most cases, the methods used to estimate both 1980 and 1981 allowed the detection of significant differences among genotypes using only two and three replications in 1980 and 1981, respectively.

In 1980, significant differences for 1980 were detected among genotypes within crosses (Table 3.1). Highly significant differences for 1980 were detected among genotypes assembled from both sources (Table 3.2). In 1981 differences in 1980 were significant only among the genotypes from crosses A (Tables 3.1). In 1980, significant differences for 1980 were observed when genotypes from both sources were compared (Table 3.2).

In 1982, yield differences were significant in Years 1980-81 and 1981-82 at the 0.05-0.1 and 0.1-0 levels, respectively, among the genotypes that were significantly separated (Table 3.3). In 1981, yield differences were highly significant among genotypes assembled from both crosses (Table 3.3).

Table 1. Individual plant growth rates (mm/d), seed germination rate in 1980, and seed germination rate in 1981, of 17 soybean genotypes from two collections in 1981.

Genotypes	1980		1981
	Replanted at day mean ^a	before 8 day TEST 13-0-0-0	
Replanted			
RR1000	0.714, 0.714	0.714, 0.7	2.250, 2.250
RR1000	4.034, 3.9	3.913, 3.9	2.248, 2.248
PTT-1.111	4.124, 3.9	4.124, 3.9	2.213, 2.213
PTT-1.114	0.714, *	0.714, 0.7	2.213, 2.213
PTT-1.412	4.143, 3.9	4.143, 3.9	2.149, 2.149
PTT-1.413	4.111, 3.9	4.111, 3.9	2.149, 2.149
PTT-1.415	3.711, 3.9	3.711, 3.9	2.149, 2.149
PTT-1.416	3.711, *	3.711, *	2.147, 2.147
PTT-1.418	3.711, *	3.711, *	2.147, 2.147
Mean	4.148	3.914	2.213
CV	0.004	0.123	0.113
SL-412,	PTT-1.3	PTT-1.3	PTT-1.3
Before 8 day			
Replanted	0.714, 3.9	0.714, 3.9	2.150, 2.150
RR1000	4.034, 3.9	3.913, 3.9	2.248, 2.248
PTT-0.911	3.913, 3.9	3.913, 3.9	2.248, 2.248
PTT-1.414	4.113, 3.9	4.113, 3.9	2.148, 2.148
PTT-1.417	4.143, 3.9	4.143, 3.9	2.149, 2.149
PTT-1.420	4.143, 3.9	4.143, 3.9	2.149, 2.149
PTT-1.421	4.113, 3.9	4.113, 3.9	2.148, 2.148
PTT-1.511	4.034, 3.9	4.034, 3.9	2.141, 2.141
PTT-1.512	4.034, 3.9	4.034, 3.9	2.141, 2.141
Mean	4.133	3.943	2.149
CV	0.009	0.147	0.113
SL-412,	PTT-1.3	PTT-1.3	PTT-1.3

(*) Means followed by the same letters are not significantly different at P=0.05 level.

Table 2.1.2. Definitions used during 1980-81, based directly from a Land area listing report, and used jointly by all agencies in systematic planning. From the California Resources Agency and Resources & Energy in Table 10.

(ii) Books published by the same Author are also copyrighted.
differences are negligible.

Differences across environments were approached. The DGR with mean weights in 1989 82-0-1-8 (Table 3-3). The weights by environment interactions effects were non-significant for DGR and RGR, but nearly significant (P=0.05) for yield, among the four sets of genotypes in Table 3-2(a)-(d). Thus DGR and RGR exhibited more variability than yield across environments.

Relationship Between Differential Yield Coefficient Ratio and Yield

Genotypes that exhibited higher DGR tended to have higher relative biomass and weight (Table 3-4). However, the magnitude of the positive correlation between DGR and yield was different among experiments.

The positive correlation between DGR and RGR was significant in two of three experiments (Table 3-4), but only a small portion of the variation in RGR could be attributed to DGR as shown by the relatively low correlation coefficient. These results are interpreted to suggest that genotypes which grew more buds per unit area tended to exhibit higher DGR, or vice versa.

Relationships between DGR on a whole plant basis and seed yield were similar to that reported by Kaji (1978). In two of three experiments, the positive correlations were present between DGR and seed yield (Table 3-4). In the 82-0-1-8 there was evidence were not associated; therefore, DGR appears to be a poor yield-increasing factor using

Table 3-1. Mean squares from the analysis of variance for individual seed germination (SG), seed growth rate (mm day^{-1}) and seed mass (SM), and mean plant height measured F2 progenies across factors F1-G-1-2 and F1-G-3.

Source of Variation	SG	SGGR	SM	MPLH
Environment	1	157.2	114.2	72.029
Blocks (Env.)	1	55.0	44.2	16.076
Genotypes	9	81.418	101.9	44.700
Env. \times Env.	9	12.7	81.7	32.004 (1)
Error	15	11.8	111.6	9.619

(1) = 121. Significance at P<0.01 and P<0.05 levels.
respectively

Table 5. Correlation coefficients (n = 1000) between harvested seed growth rate (HSGR) and either GTRD, and between natural harvested seed weight (NHST) and seed yield in three experiments.

Treat.	Rate		
	R _{HSGR-HSGR}	R _{HSGR-GTRD}	R _{HSGR-NHST}
HSGR vs. HSGR	0.48	0.21*	0.19**
HSGR vs. GTRD	0.15*	0.30	0.47*
HSGR vs. NHST	0.19	0.16	0.20
NHST vs. HSGR	0.26*	0.03	0.26**

* $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$, respectively.

genotypes from three countries.

Correlations between plant yield and SGR were positive but not significant in all experiments (Table 3.4). Consequently it appears that yield was more closely associated with seed number per unit of root area.

Relationship between plant TGR and mean sowing rate on a fixed Area Basis

Contrary to some previous results (Macy and others, 1974; Taylor and Miller, 1974) and this and Legge (1976), a positive and highly significant association between yield and SGR was observed among all the genotypes (Fig. 3.1). The linear regression of yield as a function of SGR explained 61% of the yield variation.

In all cases, field results confirmed the prediction of the simulations. In each experiment most of the yield differences were explained by the linear regression of yield as a function of SGR (Fig. 3.2, 3.3, and 3.4). However, yield as a function of mean sowing rate was not and did not fit a function of SGR alone (seed number). Since seed number is a component of both yield and SGR, these two values are not statistically independent. Thus, according to R^2 values (correlation and R^2 values were undetermined except the relationship between yield and SGR was apparent even among the genotypes in Test 13-0-2-9 (Fig. 3.1), where SGR values ranged from about 0.16 to 0.24 kg/day/ha, i.e. were not significantly different among genotypes (Table 3.1)). In

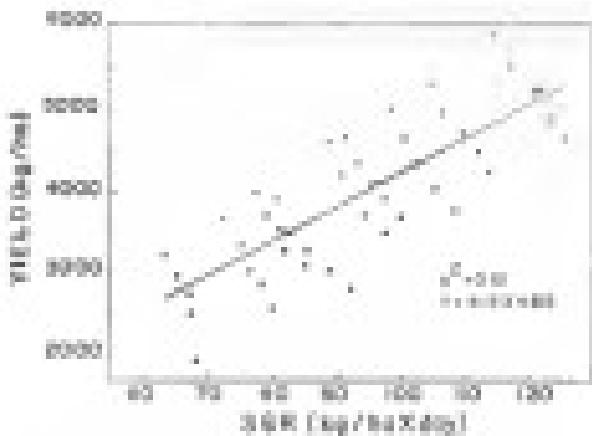


Figure 9.3: Association between seed yield and Rainfall Rate on a land area basis (1992) among simulated soybean genotypes.

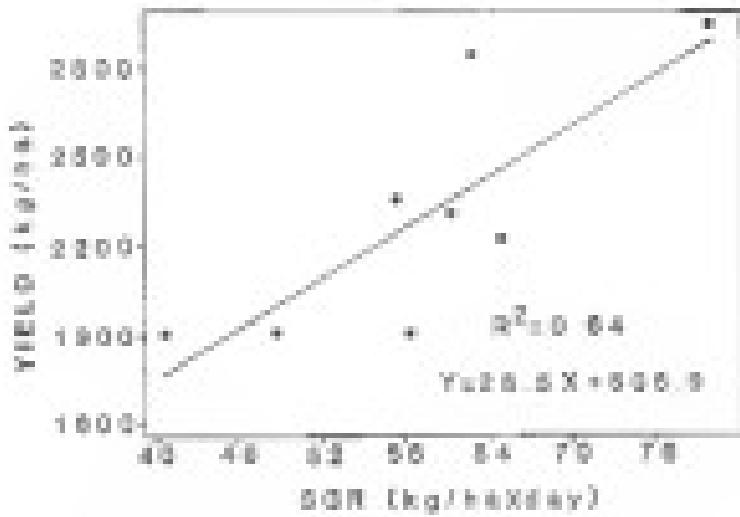


Figure 4.3. Relationship between seed production and breed growth rate in a land race banana variety having different genotypes as described in Table 4.2.

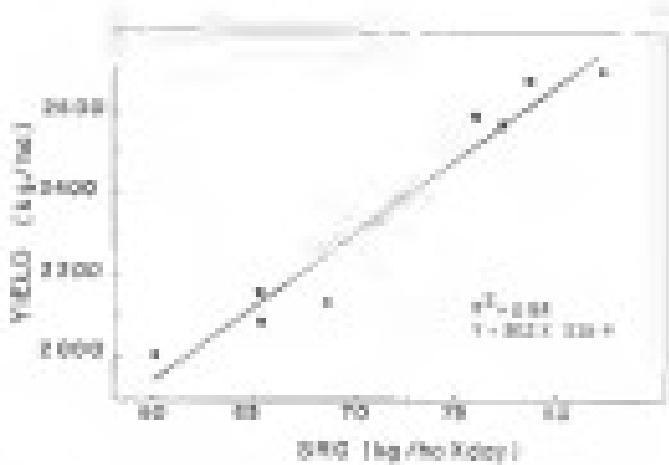


Figure 5.24: Relationship between seed yield and seed C:N ratio for a total of 2000 accessions among soybean genotypes in Brazil (Santos et al., 2007).

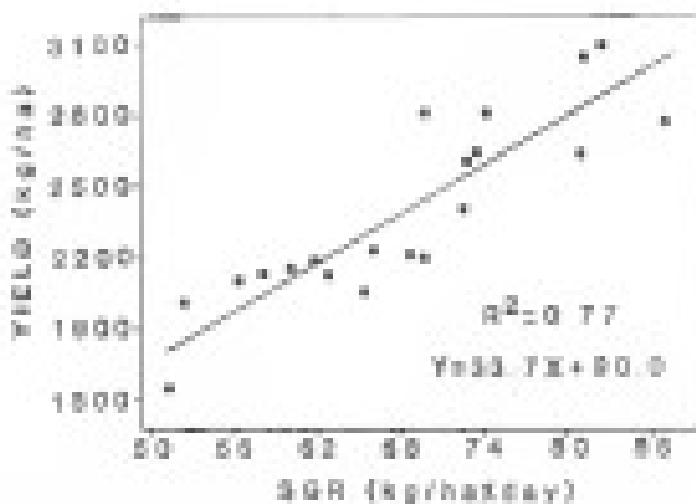


Figure 3.4: Relationship between seed yield and Seed Growth Rate in a 'Lerd' wheat variety (2000 winter wheat genotypes in total, 13-2-1).

these studies, the relationship between yield and RGR was generally strong, genotypes closest to expected parental combinations, both associations and hybrids contribute as well as the lack of a strong association between yield and different estimates of the tillage period among various genotypes (chapter IV) supports the idea that yield was mainly a function of RGR.

Effects of Tillage on Association Between Yield and RGR

Most of the yield variation among simulated and field grown soybean genotypes was explained by differences in RGR, the yield of yield as a function of RGR. In which the characterization of each of 18 simulated genotypes and their RGR (Fig. 3.8), provides the opportunity to examine which factors were mainly responsible for this close association as previously shown in Fig. 3.1. The R^2 value for the linear model was 0.73, the highest yield yield was observed in the simulated genotype which simultaneously presented a combination of the highest RGR and PGR, with the lowest RGC, and one of the highest RGR (Fig. 3.8). Conversely, the lowest yield yield was observed in the simulated genotype with the lowest RGR and PGR, the highest RGC, and almost the lowest RGR.

Within a given PGR and RGR level, yield and RGR increased linearly as a function of RGRR in simulated genotypes (Fig. 3.8). Field results also show (Fig. 3.9)

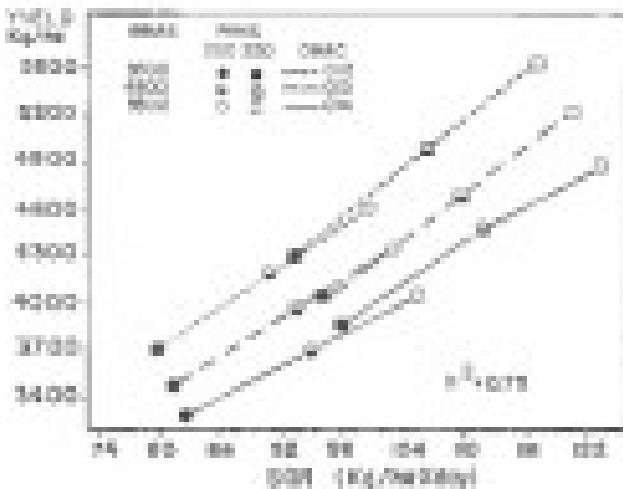


Figure 5.5 Factors influencing the relationship between seed production and basal crown ratio (%) of pure stands (OMA) among 12 labelled eucalyptus species.

supported this hypothesis. Correlations were significant ($p<0.05$) between seed yield and DMAD, and weaker ($p>0.05$) between DSI and DMAD. The LAI values at the beginning of seed growth in the simulations were approximately 3.0, 3.1, and 3.2, respectively, when DMAD values were 0.00, 0.05, and 0.10 kg/m². Shattock and Rymer (1995) observed a linear increase in dry matter production with increases in seed dormancy interpretation at similar LAI values. Therefore, the yields increased in the simulations due to increases in DMAD should be attributed to greater water resource interpretation, and to additional assimilates that may be mobilized to seeds.

In the simulations decreases in DMAD resulted in yield and LAI increases only when the DMAD levels were balanced or increased and DMAD levels were balanced or decreased (Fig. 5.10). An example of the possible interactions among these factors are the two genotypes that created yields of 3200 kg/ha by 1990 through different combinations of these three factors. Thus, similar yield levels can be reached through different means. The lack of yield increases with DMAD increases when other factors changed, suggests a possible regulation by the relatively large portion of the yield which was controlled by the reduction in seed dormancy. This agrees with several previous research reported by Rymer et al. (1995).

Simulations suggest that reduction for higher DMAD among genotypes of similar DMAD and DMAC levels would

result in higher plant levels (Fig. 5.5). Since PGR is the rate of potential source per basal production of the developing crop (photophytes), the selection proposed above would result from higher photosynthetic rates at a basal area basis.

Differences in DMAC at a given DMAD and DMF level among selected genotypes produced a similar small decrease in DM DM if there is strong evidence in field due to increases in the duration of seed filling (Fig. 5.3). The strong negative correlation between DMF and differences estimates of the duration of seed filling (DMF, DM₀ and DM-DM) observed in field-grown hybrid genotypes (Chapter VII) supports this hypothesis. These results suggest that lower DMAD values may be caused by experimental wheat having longer seed filling periods, and higher yields are measured.

Four selected genotypes exhibited essentially similar DM DM to DM₀/DM₀ ratio while their plants differed by almost 25% (Fig. 5.5). It appears that the yield differences between these genotypes were mainly due to DMAD differences. Thus, DMAD differences may be one of the factors related to the yield differences observed in these three same genotypes of Italian wheats. In this case DMAD differences could be related to differences in the length of seed filling.

Discussion

The methods used remained true in a whole plant context, and were rather precisely. The CV's were about half the magnitude of those previously reported for dry weight traits. Significant differences for CCR and GCR were detected in more cases than only two or three experiments. Differences in GCR were non-significant in only one of three experiments.

Differences in seed growth rate and size showed greater variability than plant growth components. Excepted by interaction, interaction effects were not significant for LGR and GCR but were highly significant (P<0.01) for yield, among the genotypes studied.

Seed yield had very positive associations with GCR in all genotypes from two crosses. Genotypes that exhibited higher GCR tended to have greater seed yield weight. In one of three experiments, about half of the yield variation was explained by GCR, and consequently most of the yield variation in the other experiments could be attributed to variation in the number of seeds per unit area.

Contrary to our studies in which different experiments were used, simulations predicted a positive and highly significant association between seed yield and GCR. In all cases, first results confirmed such prediction. Most of the yield variation was explained by the linear regression

of yield as a function of PGR. The lack of a strong correlation between plant and PGR observed in Chapter 10 among the pure genotypes also supports the idea that seed yield was primarily a function of PGR.

Increases in PGR and PGR tended to increase yield and PGR, while CRAC increases tended to decrease both yield and PGR among selected genotypes. Yield results in Table 10B10 support this hypothesis. Below, yield losses can be detected through several pathways due to the interaction of three factors and the length of seed cutting. But the highest yields were observed in the selected genotype with longest seed cutting period, lowest PGR, and almost the highest PGR.

CHAPTER VI
ASSOCIATIONS OF DRY MATTER ALLOCATION (DMAL) WITH
YIELD, LEAVES OR STEM PELTING, AND OTHER TRAITS

INTRODUCTION

Dry Matter Allocation Coefficient (DMAC) is defined as the ratio of linear harvest index (LIH) increase of soybean during seed filling, over its 100% maximum corresponding filling leaves (Maltezovska et al., 1994). Index RI is the ratio of mean dry weight to total plant dry weight. DMAC characterizes the rate at which dry matter is allocated or partitioned to seeds during seed filling.

A negative but nonadditive association between yield and DMAC was observed among major soybean genotypes of different maturity classes (Maltezovska et al., 1994). The weak negative association between yield and yield is important, because it indicates that yield may be governed by a DMAC value, as the capacity of assimilates stored in vegetative organs. If this pattern is corroborated in soybean plants, DMAC may be a yield-limiting factor. The type and strength of the association between yield and DMAC should be determined further among random genotypes within species.

Silveira-Santos et al. (1996) observed that the highest seedling emergence tended to coincide both low DAW and high seed germination (95%) on a sand area (soil). More information is needed on this subject to better understand the relationship of these two parameters that ultimately lead to soybean yield.

Field emergence depends on soil and the duration of the seed filling period. It follows that factors limiting sowing rate at the duration of seed filling may also limit seed yield. Siqueira and de Souza (1979) hypothesized that the high emergence density at soybean seeds can be due to higher protein concentration, relating to other crops. Since the length of the seed filling period and yield of soybeans, information is needed on the association of seed protein percentage and the length of seed filling to soybeans that would indicate LF as the primary basis of the relationship between emergence.

Silveira-Santos et al. (1996) observed a strong negative relationship between DAW and the length of the filling period (LF-ST) in eight genotypes of different origin. Thus it appears that high DAW values are another factor that limits the length of seed seed filling in soybeans.

The basis for the negative relationship between seed and seed filling duration has not been clearly determined. Silveira-Santos et al. (1996) reported a positive correlation between seed and seed protein percentage in a limited

number of genotypes. Studies on this subject should be done using random genotypes would generate no adequately accurate results with physicians.

The following approach was used in this work:

- 1) Hypotheses about the association of BMAC with pasti, ROR, and child period nutrition were tested using the cumulative total of various representative growth described in Chapter III. In resulting hypotheses were tested using new and random 17 different genotypes from two sources, in two years.

Objectives of this work were: 1) to determine the significance of the association of BMAC with yield mean random genotypes, 2) to determine the peak associations of BMAC and ROR to pasti using selected genotypes, and 3) to determine the relationships among BMAC, and child growth, and child protein percentage in random genotypes. Additional objectives were to examine additional factors which influence the association of BMAC with the length of child's illness, and to evaluate the feasibility of BMAC among physicians and the broad range variability.

Material and methods

The 45 simulated northern genotypes described in Chapter IV were used to examine hypotheses about the relationship of BMAC with pasti, ROR, and child feeding variables (RPP and RPR). Simulated data were fitted to linear regression models to determine the

Hypotheses that were subsequently tested in this experience.

The materials and methods used in the field experiments are described in previous chapters. Survival data from four field experiments (Tables 8.2-8.4) of, 8.1(a)(b), 8.1(c)(d), and 8.1(d)-(f) are presented in this chapter. The first two experiments and the last one were crop growth analysis in which DMG, GGR, RGR, and LRR were measured in relation to yield, seed protein percentage, and the length of the period 8.1-8.2. Test 8.1-c-(d) was intended only to determine yields, seed protein percentage, and RGR.

Results and discussion

8.1. Yield differences (efficiencies) from two experiments

In 1983, highly significant differences in DMG recorded from the sampling dates and seed yield were observed among 44 genotypes from each series (Tables 8.1(a)-(b) and 8.1(d)-(f)). Average DMG and seed yield of the genotypes from each series are presented in Table 8.1 along with other statistics for these two years. In 1984, highly significant DMG differences were observed in Test 8.1-c-(d), among a total of 48 genotypes from both crosses which included the respective parents (Table 8.2). Similar DMG differences were also observed in 1983 within each series. In the 48 genotypes that were recorded in 1983 (Table 8.2), highly significant yield differences were observed in

Table 6.1 Mean, standard and standard errors, and standard deviation of DMAC and seed yield of 16 random F2 progenies from two crosses and their respective parents in 1983.

	Parents X (parents)		Parents x (F2) (F2)	
	Mean	SEME	DMAC	Yield
	day ⁻¹	kg/ha	kg/day	kg/ha
Mean	8.8132	0.043	0.0210	2187
Max. value	8.8132	0.012	0.0210	2194
Min. value	8.8107	0.011	0.0208	2181
Stand. Dev.	0.0001	0.00	0.0010	318

Table 4-3 City Building Allowances (from LC-Labs, 1992) as Labeled by LC-Labs (see LC-Codes.org), 12-0-0-0-0, and 12-0-0-0-1.

very similar among the 20 genotypes from both sources which included the respective parents. Average yield was 2150 kg/ha, and the highest and lowest yields were 2184 kg/ha and 1457 kg/ha, respectively, for FTB-129 and FTB-6210.

In 1992, DMG for DMG were 0.884 and 0.875, respectively, in lines 01-6-1-8 and 10-0-2-7. Calculations were based on 10 genotypes per source, two replications per genotype, two sampling dates per replication, and three plants per sampling date. In 1993, estimates of DMG based on the same procedure but from three replications per genotype had a difference. Cramer et al. (1993) reported considerably more bias in DMG for a number of dry weight traits from numbered and genotypic analyses. Therefore, considerably less sampling effort and resolution of material would be required to estimate DMG at a given generation level, compared with other dry weight traits.

Relationship Between Dry Weight Allocation Coefficients and DMG (%)

A negative association between DMG and seed yield among advanced release genotypes was predicted from data generated by the author (Table 4.2). Results of field experiments performed in two years on a number of genotypes from two sources support this hypothesis. In all cases the correlations between DMG and seed yield were negative (Table 4.2). The associations between DMG and seed yield being significant and field grown ratios and densities

Table 4.3. Phenotypic correlation coefficients in between Dry Matter Accumulation coefficients (DMAC) with total seed yields and DMAC in simulated and field grown soybean genotypes from two sources.

TENURE	EFFECTS AND GENOTYPES (n=93)	1983		1984	
		ESTIMATED	MEASURED	ESTIMATED	MEASURED
		N	S.E.D.	N	S.E.D.
DMAC vs. yield	-0.41**	-0.13	-0.17	-0.42	-0.13
DMAC vs. SPP	-0.31**	-0.16**	-0.27**	-0.32**	-0.16**
DMAC vs. SDS-SDG	-	-0.16*	-0.21*	-0.16**	-0.16**

*,** Significant at 1% and 5%, levels, respectively.

genotypes were similar at the time of sowing (Mitra et al., 1994).

Final yield and partition by Pather Alluvium
Cultivation, soil depth, SOC and crop variety

Seed yield tends to significantly raise the contribution of the associated parameter, partitioning of assimilates from vegetative to reproductive stages and seed dry weight accumulation per unit of land area. Since DMG reflects the rate of partitioning of assimilates estimated as dry matter, the proportion of yield as a function of DMG and SOC may capture some of the yield variation in a population of genotypes. The results observed in simulated genotypes support this hypothesis. All the yield variations can be explained by the regression on DMG and SOC (Fig. 4-2). The resulting response surface was a plane which shows that simulated genotypes with the highest yields were the ones with high SOC and low DMG values.

Due to field grown wheat genotypes from the crosses (BIRRI 81-0-1) tested along spectrum with the ones predicted by simulated genotypes for the regulation of yield as a function of DMG and SOC (Fig. 4-2), variance revealed more variation in these BIRRI-11, in that BIRRI-11 the total effect was insignificant.

In addition, when depths were higher, the daily number of plant assimilate was less and sufficient to maintain SOC SOC is diminished. Consequently, more assimilate were

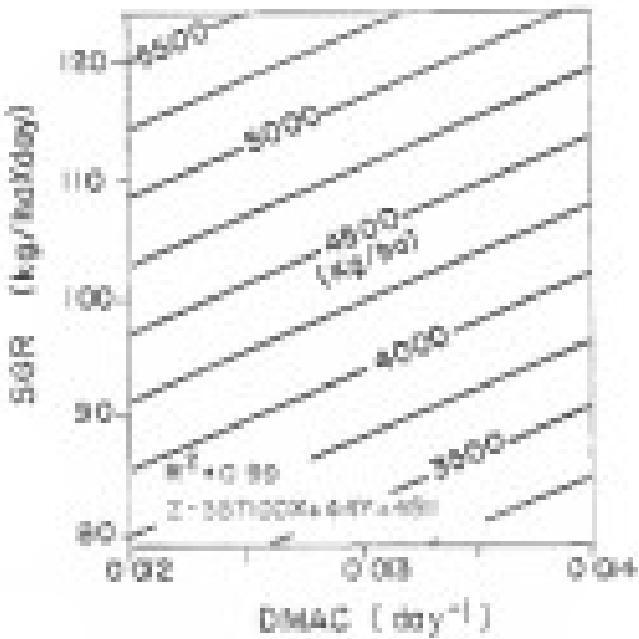


Figure 8.3 Seed yield as a function of the Day Rate. At Loughlinstown, Dublin (Fitzgerald, 1990) and Seed Growth Rate on a LAD basis (data kindly supplied by AgriSearch Research Station).

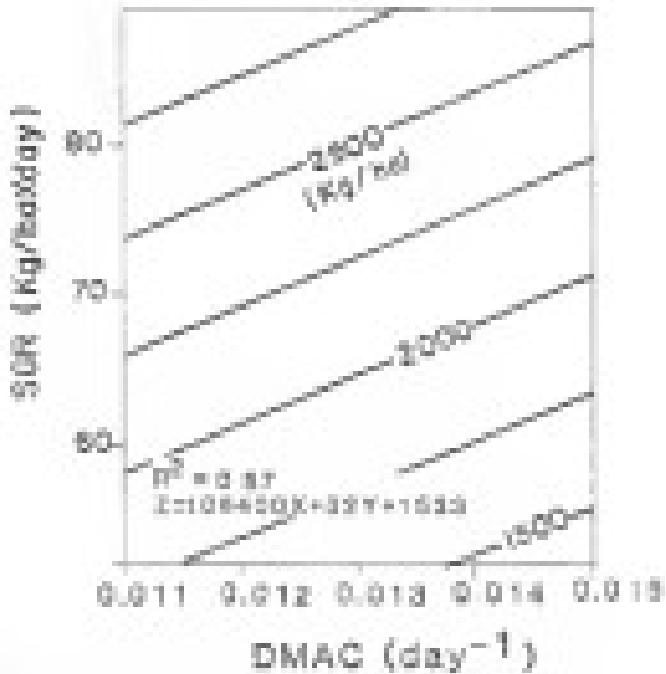


Figure 8.4: Seed yield as a function of the Day Neutral Allometric Coefficient (DMAC) and seed growth rate in a field crop maize (Zea mays L.) under different seed density genotypes in test 8.3-a.

translocated from vegetation to reproductive organs by way of some SOC elements, causing depletion of vegetative structures. Whether this effect is fluid green sulphur is mainly due to the heterotrophy of *S.* or process of the bacteria and/or the fungi, still, at the moment, is not clear, should be determined. However the nature of the anti-faecal mechanism, these results support the idea that this mechanism exists during seed falling in the aridland plant.

Association of the highest efficiencies of different *SOB* with different *EPF* in presence of *SOA* and *SOB*

A strong negative association between EPF and SOA was predicted by the simulated various genotypes (Fig. 3). These data were generated by combining a combination of five *SOA*'s with three *SOB*'s in the sequencing of seed growth curve (Fig. 3). Results from our field experiments, such with eight selected determinants of sulphur quaternary from the crosses *Rosmaria x Rosmaria* x *EPF-100* in one year, and 20 selected genotypes in another year, partially support the hypothesis formulated with the model. In 1989, the correlation coefficients between EPF and each were $r=0.811$ (solid) and $r=0.784$ (open), respectively for *Rosmaria* x *Rosmaria* and *EPF-2-3-8*. The positive correlation in *Rosmaria* x *Rosmaria* may be an artifact caused by the small range in EPF (0.1 to 1.0 degree). In 1990, a significant association

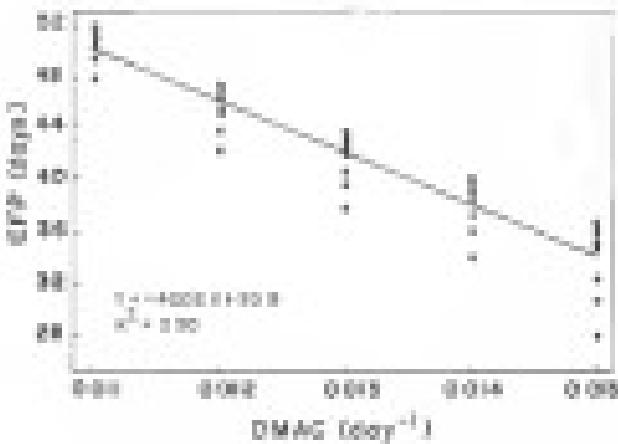


Figure 4.4: Estimated Evapotranspiration Period (ETP) as a function of DMAG (day⁻¹) At Jalan Sungai Putih (JSP), using simulated regional groundwater flowpath.

between DPP and DMAC was observed in that 85-0-0 (Fig. 14).

By definition DPP is the ratio of final Δ to Δ_{DMC} , thus a close negative correlation between DPP and DMAC should be expected. Results from simulations and field data fully support this idea. Highly significant negative associations between DPP and DMAC were always present, and DPP differences displayed by a year across DPP differences in each experiment (Table 8.1). Furthermore, regression of DPP as a function of DMC using data from the field experiments produced a decline in Δ of 2.1 to 2.7 days for every 0.001 day⁻¹ increase in DMC observed.

In both years, the fitted results of the ranges of seed filling, 85-07, also showed significant or highly significant negative associations with DMAC, similar quantiles from two species (Table 8.1). These results further support the hypothesis that a strong negative association exists between DMAC and the duration of seed filling in soybean. It follows that DMAC influences the intensity of the seed maturation in the soybean plant, irrespective of the nature of the stimulus which may be participated in seeds.

The plot of DPP as a function of DMAC in which the characteristics of simulated genotypes are presented (Fig. 15), affects the opportunity to compare whole additional characteristics influence the strong negative association observed in field experiments and in simulated genotypes.

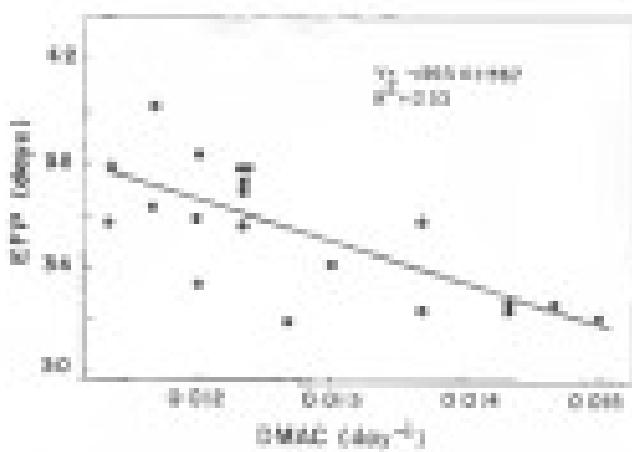


FIGURE 4-8 Effective Filtration Period (EFP) as a function of DMAC. Alluvium Coefficient (1965), using different IT prototypes in Test 61-0-2.



Figure 3.2. Factors influencing the association between intrinsic binding potential (IBP) and Oct Receptor Content (ORC) among different thyroid genotypes.

(Fig. 4-10) between these two traits, the length of EPP was probably influenced by Aligned DMAC values, and only minor changes were observed in EPP with varying DM and PGR levels in simulated genotypes. These simulation results are in agreement with the results observed for the relationship between plant and EPP (Fig. 4-10) discussed in chapter IV.

Relationships of Seed Protein Percentage and Box Scatter of Yield Components and Length of EPP

As stated before, the strong negative association between DMAC and different estimates of the length of seed filling, and the weak negative association of DMAC with yield, support the existence of a yield depressive mechanism in soybean during seed filling. The availability of random genotypes with differing seed protein percentages provided the opportunity to test whether higher seed protein percentage is a causative factor in the yield depressive mechanism as proposed by Blazquez and de Vic (1975, 1976).

Correlations of seed protein percentage with DMAC, EPO, and 85-87 were usually nonsignificant and inconsistent over experiments and crosses (Table 5-1). Correlations between seed protein percentage and DMAC were significant and negative in four (1974-1, 1975-1, 1975-2, and 1976-2), but not in 1976-1. A nearly significant positive correlation was observed. A significant negative correlation between seed protein percentage and 85-87 was observed in four (1974-1, 1975-1, 1975-2, and 1976-1). In general, correlations did not show a consistent

Table 8.4. Phenotypic correlations coefficients between seed protein parameters, by Better Alluvium
Cultivars (BAC), Reproductive traits cultivars
(RPT), and BAC.

Trait	BAC	RPT	BAC vs RPT
<hr/>			
B2-G-2-6	-0.19* (n=10)	-0.16 (n=10)	0.23 (n=10)
B2-G-2-7 ^a	-0.18 (n=10)	-0.17 (n=10)	0.30 (n=10)
B2-G-2	-	-	-0.37* (n=10)
B2-G-2	0.42** (n=10)	-0.12 (n=10)	0.74 (n=10)

* Correlation significant at 95%.
** Significant at 99.9%.

positive or negative association of soybean yield with percentage with DAD or the length of the seed filling period. The results do not provide enough evidence to support or reject the idea that it is the basis of the yield depressive mechanism that shortens the length of the soybean filling period as proposed by Sheldene and de Wet (1975, 1976). Therefore, the source of the yield depressive mechanism remains undetermined. Perhaps both *A* and *C* are energy equilibrium traits, too impossible for the yield depression of the soybean plant that appears to have plenty due to seed densities that exceed the daily supply of plant assimilates.

Relationship Between Genotypes and Yield Under Different Soil Management Conditions

The analysis of GAC across 1972 and 1973 for the genotypes free soybean x trifoliolate showed no significant year effects but nearly significant ($P=0.05$) differences among genotypes (Table 6.1), while yield exhibited a significant genotype by environment interaction effect.

The GAC of genotypes free soybean x trifoliolate showed a different behavior across environments, compared to yield. In 1972 both the genotype by environment interaction effect was significant for GAC and relationships for yield (Table 6.2).

Based upon heritability estimates the GAC were ranking at lower than the yield among the genotypes free

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“I am not going to let you do that again,” I said firmly.

main effects. Yield mean heritabilities were 0.4 and 0.38, respectively for DMAC and yield among 11 genotypes from *Sauvignon à la folie*, and 0.12 and 0.29, respectively, for DMAC and yield among 19 genotypes from *Sauvignon à l'herbe*. Therefore, selection for low yield would require replacement strategy in different environments as was already suggested by a significant genotype by environment interaction found among the genotypes from *Sauvignon à l'herbe*.

Correlations

Both yield and DMAC showed very negative associations (-0.518 to -0.631) as predicted by the additive genetic effect. The regression of yield on a function of DMAC and SOC expressed most of the yield variation among Sauvignon and Sauvignon à l'herbe genotypes. The highest yields can be observed in the region of lowest DMAC and highest SOC.

A negative association between DMAC and DMAT was predicted by classical genetics and observed in two sets of CAVIA field experiments. However increases in DMAT were primarily due to linear DMAC as reflected by the model $(0.2+0.31)$, and quadratic in DMAT expression ($0.07(0.5)$ to 0.71). Furthermore, a significant and highly significant negative association between DMAC and DMAT was found in field experiments ($p<0.001$ to <0.0001). The strong negative associations of DMAC with yield during flowering, and the weak negative associations with yield, suggest the

existence of a self-destruction mechanism in soybeans during the filling period. Genotypes that tend to allocate GE protein more dry matter more rapidly to seeds, do so at the expense of a larger share in vegetative dry matter, and shorter seed filling period.

The basis of this self-destructive mechanism remains unknown, because uncoordinated and unpredictable correlations of seed protein percentage with DMAC and seed filling duration measures did not support the idea that seed GE percentage is the primary limiting factor. It appears then, that both GE and DMAC energy requirement may be the limiting substrate concentrations in seeds.

A significant genotype by environment interaction for DMAC was detected among the genotypes from one of the environments tested. Yield under low-fertility conditions for DMAC among the genotypes from the eastern (ML-1 and ML-2) were somewhat lower than for yield (ML-3 and ML-4); therefore, selection for low DMAC would require replicated testing in different environments.

CHAPTER VIII SUMMARY AND CONCLUSIONS

Relationships between Yield and Seed Protein Percentage and Various Parameters

The overall objectives of this dissertation were to: 1) determine if the relationship between yield and seed protein percentage tends to be positive, when the high protein parent is the cross at either the higher yielding parent; b) to compare a visual estimate of seed filling (80-90%) with the physiological indicators of the length of seed filling (90% and 95%), and c) to determine the associations among yield and physiological traits such as the length of seed filling, individual seed growth rate (IGSR), seed growth rate on a leaf area basis (LGR), and the rate of dry matter addition to seeds (DMR) during seed development.

Based on data presented, the following conclusions appear to be justified. However, they may be reassessed by other studies.

Seed protein percentage can be expected to increase between yield and seed protein percentage if either higher or lower yielding parents are used as the high protein parent. Correlations between seed protein percentage and seed yield in several experiments under various and unlogged environments, from crosses where high protein parents were either the higher yielding parents, were similar in sign

and negatively to the ones reported here. High protein content were the lower yielding varieties.

Studies on yield and seed protein percentage should be performed across several environments to obtain accurate results. The signs and magnitudes of the correlations between yield and seed protein percentage shown could differ considerably across the environments, within countries. Correlations ranged from 0.01 to -0.51% in one country, and from 0.61 to -0.17% in another country.

Associations between yield and seed protein percentage across low and medium-yielding environments did not show a tendency to become consistently negative and stronger in lower yielding environments. However, the lack of high-yielding environments prevented adequately testing of the hypothesis that seed protein percentage tends to increase in low-yielding, underprivileged environments.

The amount of protein produced per unit of land area can be increased by seed yield increases, while the production of oil per unit area can be increased by either seed yield or seed oil percentage increases. In most cases, yield of protein and oil were a function of seed yield, and usually yields of protein were not associated with seed protein percentages. In 81% of 20 cases, positive correlations between yield of oil and seed oil percentage were significant or highly significant, but they if relevant were always considerably lower than those between yield of oil and seed yield.

A Reproductive and Economic Cost of Seed Filling
Damage from the Rootworm Infestation of Barley

Barley RGR increases during most of seed filling as a consequence of increasing embryo size. Between dates harvested discontinuous filling losses increased linearly with time (Fig. 1) during seed filling in all genotypes being examined, one of two periods, showed a slightly lower fit to the linear model (Fig. 1a).

Satisfactory estimates of RGR, the rate of linear RGR increase, were obtained using data from a few plants sampled twice daily and later during seed filling. Estimates of RGR based on two sampling dates can be used satisfactorily with inclusion of RGR associated non-discontinuous sampling performed at random seed filling. The CV's of RGR estimates based on two sampling dates ranged between 0.03% and 0.11% among genotypes from the 2000-01 to the 2001-02.

The linear RGR increase during most of seed filling and the positive estimates of RGR that can be obtained from two sampling dates provide the opportunity to characterize seed filling duration in a precise, reproducibly sound, and relatively inexpensive way.

Reproductive Period Duration (RPD), was defined as the difference of time in days between discontinuous filling dates (Fig. 1).

Genotype-Environment
Relationships for Yield, Number of ears,
Ears per ear, and Number of spikelets per spike

YIELDERS of year 1968 at a maize plant breeder obtained from only one entry and one late sampling date can be used satisfactorily with estimates of EPP obtained from sequential samplings performed throughout each filling date or 1968 obtained from two samplings plus mature individual plant weights can be used to calculate EPP with relatively low CV's.

In all cases, year 1968 and EPP converted simultaneously to biomass dry-weight quantities from the entries. Plants reached 85-90 kg/ha before either EPP or EPL, but differences among these three stages were positive and strong (P<0.01). Although it has an important influence of EPL and EPP on determinants of yield, it was an acceptably precise relative measure.

Year 1969 at a maize plant breeder had reached more in the stage after year 1968 in each genotype-environment combination, and plants lost vegetative dry weight after EPL was reached. In two of three cases, differences between EPL and EPP were significant, though it was an increase and perhaps because of EPL in two of three experiments by different maize genets.

Differences for EPL, EPP, and EPL can be found among different genotypes. In all cases, highly significant differences for EPL and EPP were observed within experiments, while highly significant differences for EPL

more advanced only in one of three experiments.

The association between age and ADF was positive but not consistently significant, because both periods showed some linear but non-significant trend for three to seven days younger.

The visual estimate of the length of seed fallows, 85-87, was not a consistent, precise, and accurate estimate of either EPP or EPO, because the period 85-87 was 4 to 11 days longer than EPP, and slightly longer than EPO, using a number of determinants previously from the census.

The use of EPP, EPO or 85-87 as selection criterion in defining biomass appears to be limited to some extent due to the significant or highly significant positive or negative associations and low levels some correlations that can be observed for these criteria.

Assessment of a Simulated Soil-Crop System Model

A simple simulation model of soybean reproduction growth was developed. The model is based on the assumption that seeds prove to seed green their seed yield only if the latter has reproductive dry weight varieties can tolerate and develop of seed. The primary players in the model are an annual system that have particularities in regions having either the dry or wet soybean climate.

The model incorporates C₃ canopy height after the onset of vegetative reproductive growth, depth to the soil surface (mm), root, and shoot biomass production and root percentages as well as vegetative R percentage can also be simulated. Outputs of the model on a daily basis are leaf, temperature, and total dry weight (g), EC, RH, and root respiration rates. The model estimates the simulation when LCC becomes negligible and plants are assumed to be mature. At crop maturity the model outputs include total final RT and PGR. Estimated filling period can be calculated as the ratio of final root weight to root during the linear portion of simulated root growth.

ASSOCIATION OF YIELD WITH ROOT PHENOLOGY AND NODAL FILLING IN POTTED PLANT GROWING

Statistical analysis and field experiments with P. myricoides genotypes show that weak positive associations have been observed between yield and both PPF and PGR within environments. The linear regression model of yield as a function of either PPF, PGR, or PPF multiplied with PGR portion of the yield differences among genotypes within environments.

Relations for long filling periods (PPF, PGR, and PPF×PGR) data are considerably results in association for higher yields within environments, because both quantities with long root filling periods had the positive correlation although, genotypes with short root filling periods usually

had high yields. The R^2 values can be somewhat higher in experiments where genotypes evaluated by separate differences in yield and seed filling period estimates are used. In those cases, variations in RGR-RD explained about 60% of the yield variation. These results indicate research that seed growth rate on a leaf-area basis may be a more appropriate yield-determining factor than seed filling duration in maize inbreds genotypes.

The weak positive associations observed between yield and different estimates of the length of seed filling can be explained by the differential influence that RGR had on yield and RGR away from seed genotype. Within a given RGR level, increases in RGR and RRD produced sharp yield increases, but RGR remained essentially constant, while RGR decreases (i.e., negative RGR and RRD) produced a moderate reduction in yield and a large reduction in RGR.

Associations Between Yield and Seed Length Filled by Different Seed Growth Rates

Individual seed growth rate on a whole plant basis and RGR can be estimated rather precisely using a new method, although RGR estimates in this case are not substantially independent of yield. The CV's for RGR can be about half the magnitude of those previously reported for dry weight ratios. In other systems crop growth analysis, similar relationships for RGR and RRD can be detected

among four or three replicates. Differences in RGR were magnified in only one of three experiments.

Individual seed growth rate and RGR showed greater stability than yield across environments. Effects by environment interaction effects were not significant for RGR and RGR but were nearly significant ($p=0.06$) for yield in one case, among the genotypes studied.

Weak positive associations between yield and RGR can be observed. Genotypes that exhibited higher RGR tended to have higher relative individual seed weight. In one of three experiments, about half of the yield variation was explained by relative seed weight. Similarly, only in one of three experiments about half of the variation in RGR could be attributed to RGR. Consequently, most of the variation in yield and RGR in the other experiments could be attributed to fixed and random per se effect of land area.

Contrary to some reports in which released varieties were studied, a positive and highly significant association between seed yield and RGR was observed among evaluated genotypes. In all cases, dual curves among genotypes from two crosses confirmed such prediction. Most of the yield variation was explained by the linear expression of yield as a function of RGR.

The strong positive association between yield and RGR can presumably be explained by the relationships that DMR and PRAS had, with yield and RGR of evaluated genotypes. Yield and RGR increased with increasing in DMR and PRAS

longer; smaller changes in yield and size were observed with changes in PGR, while yield increased, size tended to decrease but yield decreased. The decreases in yield observed can be attributed to shorter seed filling periods.

When PGR or TBAE increased, sharp yield increases were observed only if all other factors remained constant among simulated genotypes.

Interaction of day length, nitrogen concentration, PGR and TBAE on plant height, seed yield and seed size.

Seed yield and TBAE showed weak negative associations ($r^2=0.10$ to -0.45) in field experiments that were predicted by the model ($r^2=0.07$). The regression of yield as a function of TBAE and PGR explained most of the yield variation among simulated and field grown soybean genotypes. The relationship response surface was a plane in which the highest yields can be observed in the region of lowest TBAE and highest PGR values.

A negative correlation between PGR and TBAE was predicted by the simulated genotypes and observed in two of three field experiments. Increases in PGR were primarily due to lower TBAE values as predicted by the simulations ($r^2=0.12$), and confirmed in field experiments ($r^2=0.41$ to -0.30). Furthermore, a significant and highly significant negative correlation between TBAE and H_1-H_2 was found in field experiments ($r=-0.348$ to -0.484^{**}). Similar changes in H_1-H_2 were observed when changes in TBAE and PGR

more advanced genotypes. Since DMAC influences the rate of dry matter allocated to partitioned to seeds from vegetative organs, the above results indicate that earlier filling periods are positively associated with delayed depletion of vegetative dry matter during seed filling. This supports the idea that a self-destructive mechanism of seed maturation exists in soybean plants.

The basis of the self-destructive mechanism remains undetermined, due to non-significant and insignificant associations of seed protein percentage with DMAC and the length of seed filling observed in field grown soybeans. Perhaps the self-destructive mechanism is based on the energy requirements of both the C and N compounds that are transferred from vegetative tissues to vegetative seeds.

Selection for lower seed water content resulted in higher seed environments, due to significant genotype by environment interactions and lower water requirements of slightly lower than dry seeds.

ACKNOWLEDGMENT

Highest relative yield levels can be obtained by selected genotypes with different combinations of DMAC, PNAE, and DMG. These data on DMAC and DMG were in close agreement with their predictions. Therefore, maximum yield levels could be obtained by several different pathways. However, the highest yield was observed only in the

involving genotype with highest IGRAS, highest PGRS, and nearly the highest RGR that subsequently exhibited the lowest CRAC and highest GPF.

Based on previous field simulations and field experiments it appears that more theoretical approaches to increase yields are possible and can be pursued separately or in combination (Table 7.1). These approaches are (i) to increase IGRAS, (ii) to decrease PGRS, and (iii) to lower RGRs. Reducing the yield could be accomplished with reference to any one of the proposed traits, to ensure that the other traits do not decline and become limiting factors.

A fourth approach would be to reduce the higher RGR, which is not possible and highly associated with yield. But as shown in Table 7.1 reductions in either higher IGRAS or PGR would increase GPF and consequently yield.

It is obvious that a crop requires a certain minimum biomass level to support most of the other radiation and support root growth. Radiation pressure (IGRAS) that would result in 10% excess above the minimum required for minimal light compensation would tend to increase yield because of the greater availability of resources that potentially could be partitioned to seeds. Yield increases would be mainly due to seed numbers, and the length of seed strings should remain essentially unchanged. This strategy has been successfully applied to increase yield through increases in plant densities and narrow gene spacing (Liu et al., 1991).

TABLE 1.1. Apparatus to measure soybean seed viability through breeding.

TYPE or Labeled Date	TESTS OF VIGOR OR SEED VIABILITY		
	SOY	SPR	Days from planting to maturity
STANDARD TESTS	+	-	-
GRASSHOPPER TESTS	-	-	-
LOWEST GRADE	-	-	-

TEST = INSECTICIDE; - = UNKNOWN; + = THE PESTICIDE.

increases in CBRG could be minimal since, as a general action, higher yielding would result in increases with larger plant size as reported by Dallal and Gherbi (1979) and Bower (1971), and probably no much land is available.

Selection for higher PGR would tend to increase yields in plants of similar size and PGR. This type of approach would increase yield mainly due to the increases and thus would be especially applicable to soybeans since the length of seed filling and the growing period of the crop could not be substantially extended. Selection for yield would likely be the more efficient way to enhance PGR if land and time are held constant.

Screening CBRG entries would tend to minimize the risk of self destruction in different environments. Higher yields in this case would result primarily from differential increases in the length of seed filling and slightly lower PGR's.

Higher yielding varieties would be the ones which integrate both of the limiting factor situations and are able to maintain high conversion both of seed growth rates and larger portions of time while maintaining low rates of vegetative day number depletion time areas.

Possible Approaches to Intense Soybean Yield Screening

DeVries (1971) hypothesized three main directions for higher yield. First, yield must increase

period, as soybean plants of similar larger plant size under poor growing conditions, would tend to higher yields. The results of this work are in close agreement with the above hypothesis.

Relations for higher R₁ has emerged from smaller and earlier plants with lower yield (Bennet and Sherry, 1977). However, in plants of similar biomass, yield would be a function of final R₁. The correlation coefficients of yield with final R₁ was +0.92^{**} (with) among simulated genotypes with PGRs of 4000 kg/ha, three PRAC levels (150, 300, and 300 kg/ha/ha), and five PGR levels (10.00, 8.00, 6.00, 4.00, and 2.00 kg⁻²/ha). Therefore, in plants of similar large biomass competing with each other more effectively, R₁ would be a favorable selection criterion. In this case, the stability of the average plant sizes and correlations reported by Bennett et al. (1978) would be advantageous.

Assessments among simulated genotypes indicate that selection for high final R₁ among plants of similar biomass would largely increase efficiency for higher PRAC, longer and taller plant, and higher R₁. The correlation coefficients of final R₁ were +0.89^{**} with PRAC, +0.79^{*} with PGR, 0.73^{*} with PGR, and 0.61^{**} with PGR among the 15 simulated genotypes with PGRs of 4000 kg/ha that were mentioned above.

It has shown in chapter IV that taller plants were considerably preferred as PRAC decreased and PGR increased.

among classified genotypes of barley (1930 kg/ha) BMAC 1000. However, to improve the chance of selecting the highest yielding genotypes, selection for lower BMAC should be carried out in addition to selection for higher yield. It is plains of earlier biomass. The following negative correlation between final yield and BMAC (-0.34 ± 0.01) among classified genotypes with final yield of 4500 kg/ha, indicates that selection for higher yield by this will necessarily imply selection for lower BMAC. However, the close negative correlation between estimates of the length of seed filling and BMAC, reported in Chapter 11, indicates that visual selection for longer seed filling period would be a practical way to select indirectly for lower BMAC.

Combining visual selection for long seed filling period and high yield in plains of earlier biomass would convert the tendency toward earlier maturity away from more toward higher St. It has observed by Russell and Murray (1977).

Visual selection of genotypes with high, approximately 1000 kg/ha biomass at maturity, would probably be effective for breeding purposes. For whole cereal of selection for high earlier biomass, long filling period, and low St would be possible using only direct yield-based trait, instead of yield as an usually necessary when testing for yield should. Therefore, higher number of traits could be indirectly screened for yield in this way, in the way

which are causing the great unrest. In my view, to determine the advantages of this methodology over the conventional selection for plant, under practical breeding conditions, is one of the greatest scientific challenges of modern breeding.

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and I think Salado became over June 25 December 1948 by
Government, Argentina. He attended primary school there at
Colonia Belgrano where he is resident and graduated from High
School from Colegio Nacional Luis Beltrán in 1956. In 1960
he started a three year course of study at Universidad
Nacional de Tucumán, in Argentina, where he graduated as
Ingeniero Agrónomo in May 1971.

Pron (1971) stated LPPF to support its dry land research and its contribution as the Agency Department of the University of Malaya in the Tropics. In September 1971 he joined the National Institute for Agrobiological Research (NIAR) in Kepala Batang, at the Regional Exp. Sta., at Kuantan, Terengganu. There he conducted field research on soybean nitrogen and variety trials, and started a soybean breeding program for South Minahara regions. In 1980, he enrolled in the University of Florida where he graduated with a Master of Science in Agronomy in 1982. From then on he pursued doctoral work in Agronomy at the University of Florida. He has been married since 1971 and has a daughter, Marissa.

I certify that I have read this study and that in my opinion it conforms to acceptable standards of scholarly presentation and is fully adequate, in scope and quality, as a dissertation for the degree of Doctor of Philosophy.

Franklin H. Hinselwood

ARTHUR ELLIOTT
Professor of Psychiatry

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This dissertation was submitted to the Graduate Faculty of the College of Agriculture and to the Graduate School, and was accepted as partial fulfillment of the requirements for the degree of Doctor of Philosophy.

December 1946

Jack L. Ladd
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